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(54) Title: DNA SEQUENCES AND PLASMIDS FOR THE PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION

(57) Abstract

DNA sequences are described, that by integration in a plant genome cause the activity of the sucrose-phosphate-synthase (SPS) of the plant to be changed, plasmids, containing these DNA sequences as well as transgenic plants that by introduction of the DNA sequences causes changes in the activity of sucrose-phosphate-synthase.

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Title: DNA sequences and plasmids for the preparation of plants with changed sucrose concentration

Field of the invention

The present invention relates to DNA sequences and plasmids, containing these DNA sequences, which by integration into a plant genome, cause the activity of the sucrose-phosphate-synthase (SPS) of the plant to be changed and thus affect the sugar metabolism of the plant. The invention further relates to transgenic plants, in which through introduction of the DNA sequences, changes in the activity of the sucrose-phosphate-synthase are produced.

Sucrose is of central importance for the plant and serves many functions. For the long distance transport of photoassimilates and/or energy between various organs in plants, sucrose is almost exclusively used. The sucrose, which is transported in a specific heterotrophic organ, determines the growth and the development of this organ. Thus it is known, e.g. from EP 442 592, that transgenic plants, in which the transport away of the sucrose from the exporting leaves is inhibited by expression of an apoplastic invertase, shows a strong reduction in the growth of e.g. roots or tubers in the case of potato plants. For tobacco plants, the principal importance of sucrose as the central function for the long distance transport of energy carriers within the plant is described (von Schaewen et al, 1990, EMBO J 9: 3033-3044).

Whilst it has been clearly shown that a reduction of the amount of sucrose imported in the heterotrophic organs, such as tubers and seeds, leads to loss of yield, it is

not known whether an increase in the amount of sucrose in the photosynthetically active parts of the plant, mainly the leaves, leads to a better supply of heterotrophic organs and thus to an increase in yield.

A second central role for sucrose and/or the hexoses, glucose and fructose, derived from sucrose, is in the protection of plants against frost damage at low temperatures. Frost damage is one of the main limiting factors in agricultural productivity in the northern hemisphere. Temperatures below freezing lead to the formation of ice crystals. Since the growing ice crystals consist of pure water, water is abstracted from the cells as the temperature falls.

This dehydration has at least two potential damaging results:

a) all dissolved substances within a cell are strongly concentrated and the cell contracts following the loss of water. Highly concentrated salts and organic acids lead to membrane damage;

b) with rehydration from dew, the previously contacted cells reexpand. The cell membrane also expands again. The volume expansion puts a heavy mechanical load on the membrane.

It is thus clear that a freezing/dew cycle can lead to severe membrane damage of the cells and thus to damage to the plant.

It thus appears worth trying to hinder the freezing. One possible strategy is the increased formation of osmotically active substances in the cytosol of plant cells. This should lead to a lowering of the freezing point. Osmotically active substances include sucrose

and/or the two hexoses derived from sucrose.

The increased formation of sucrose and/or the two hexoses at low temperatures is desirable in the growing plant. Another situation can exist in the harvested parts of a plant, especially in storage. For example, in potato tubers that are stored at 4-8°C, hexoses (glucose) accumulate. It would appear to be sensible, to see this as the answer to a lowering of the temperature ("cold-sweetening").

The accumulation of sucrose and glucose has in the case of potato tubers economically undesirable results. Increased amounts of reducing sugars, such as glucose, in potatoes which are fried when preparing crisps, chips and the like, leads to an undesirable browning due to the Maillard reaction. Such products with a dark brown colour are not generally acceptable to the consumer. Further the cooking strength is strongly dependent on the content of starch and/or its breakdown products which are important in determining the quality characteristics of the potato.

In relation to the economic aspects, sucrose thus possesses three especially important functions:

1 as the transport form for the distant transport of photoassimilates,

2 as an osmotically active substance with the desirable activity of lowering the freezing point in intact, growing plants, and

3 in the undesirable formation of reducing sugars in stored harvested parts of a plant, e.g. the potato tubers, as a result of low temperatures.

The biosynthesis pathways for the formation of sucrose, either from the primary photosynthesis products (in the

leaf) or by breakdown of starch (in the storage organs e.g. of potatoes), are known. An enzyme in sucrose metabolism is sucrose-phosphate-synthase (SPS). It forms sucrose-6-phosphate from UDP-glucose and fructose-6-phosphate, which in a second step is converted to sucrose.

The isolation of SPS from maize and the cloning of a cDNA from mRNA from maize tissue is known (EP 466 995). In this application, processes for the purification of a protein such as by centrifuging of homogenates, differential precipitation and chromatography are described. A 300 times enrichment of SPS from plant tissue has been described by Salerno and Pontis (Planta 142: 41-48, 1978).

In view of the significance of SPS for carbohydrate metabolism it is questionable whether plants tolerate a reduction in SPS activity in all or in certain organs. It is especially not known, whether it is possible to produce transgenic plants with a reduced SPS activity. Also the use of SPS for the modification of the functions of sucrose for lowering the freezing point in intact plants and for the formation of reducing sugars in harvested parts is not known.

For the preparation of plants with reduced SPS activity, i.e. plants with changed sucrose concentration, it is necessary to make available an SPS coding region of such plant species, for which processes are described, whereby transgenic plants can be grown in large numbers. In as much as a reduction of SPS activity can be achieved, by selection from a large amount, the possibility exists of obtaining plants with such a phenotype. Further organ specific promoters for gene expression should exist for

the plant species, by which the possibility of an organ specific reduction of the SPS activity could be investigated.

A species which fulfils the stated requirements is *Solanum tuberosum*. The genetic modification of *Solanum tuberosum* by gene transfer using *Agrobakteria* is well described (Fraley et al., 1985, Crit Rev Plant Sci 4: 1-46). Promoters for leaf specific (Stockhaus et al., 1989, Plant Cell 1: 805-813), tuber specific (EP 375 092) and wound inducing (EP 375 091) gene expression are known.

The present invention now provides DNA sequences with which changes of SPS activity are actually and demonstrably possible and with which the sucrose concentration in the plant can be modified. It is concerned with sequences with the coding region of sucrose-phosphate-synthase (SPS) from *Solanum tuberosum*.

These DNA sequences can be introduced in plasmids and thereby combined with steering elements for expression in eukaryotic cells. Such steering elements are on the on one hand transcription promoters and on the other hand transcription terminators.

Each plasmid comprises:

a) a suitable promoter, that ensures that the coding sequence is read off at the suitable time point and/or in a specified development stage in the transgenic plants or in specified tissues of transgenic plants,

b) at leat one coding sequence, that

   i) is so coupled to the promoter that the formation of translatable RNA is allowed in a protein, whereby the protein demonstrates

enzymatic activity, that leads to a modification of the sucrose concentration in the plant, or

ii) is so coupled to the promoter that the non-coding strand is read off, which leads to the formation of a so-called "anti-sense" RNA, which suppresses the formation of the coding protein of an endogenous gene in the plant, which is involved in the sucrose biosynthesis, and

c) a non-coding termination sequence, that contains the signals for the termination and polyadenylation of the transcript.

The present invention further provides plasmids in which there are the DNA sequences which change the SPS activity in the plant.

The coding sequences named under b) are the SPS sequences with the following nucleotide sequences:

SPS 1 sequence (Seq. ID No.1):

CTATTCTCTC CCCTCCTTTT TCTCCTCTCT TCAACCCCAA AACTTCCCTT TCAAAGCCTT 60

TGCTTTCCCT TTCTCACTTA CCCAGATCAA CTAAGCCAAT TTGCTGTAGC CTCAGAAAAC 120

AGCATTCCCA GATTGAAAAA GAATCTTTTT CAGTACCCAA AAGTTGGGTT TCTCATGTCC 180

AGCAAGGATT AGCTGCTCTA GCTATTTCTT TAGCCCTTAA TTTTTGTCCA GTTGTGTCTT 240

CTGATTCTGC ATTGGCATCT GAATTTGATG TGTTAAATGA AGGGCCACCA AAGGACTCAT 300

ATGTAGTTGA TGATGCTGGT GTGCTTAGCA GGGTGACAAA GTCTGATTTG AAGGCATTGT 360

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TGTCTGATGT GGAGAAGAGA AAAGGCTTCC ACATTAATTT CATCACTGTC CGCAAGCTCA  420

CTAGCAAAGC TGATGCTTTT GAGTATGCTG ACCAAGTTTT GGAGAAGTGG TACCCTAGTG  480

TTGAACAAGG AAATGATAAG GGTATAGTTG TGCTTGTTAC AAGTCAAAAG GAAGGCGCAA  540

TAACCGGTGG CCCTGATTTT GTAAAGGCCG TTGGAGATAC TGTTCTTGAT GCTACCGTCT  600

CAGAGAACCT TCCAGTGTTG GCTACTGAAG AGAAGTACAA TGAAGCAGTT TTCAGCACTG  660

CCACACGTCT TGTTGCAGCC ATTGATGGCC TTCCTGATCC TGGTGGACCC CAACTCAAGG  720

ATAACAAAAG AGAGTCCAAC TTCAAATCCA GAGAGGAAAC TGATGAGAAA AGAGGACAAT  780

TCACACTTGT GGTTGGTGGG CTGTTAGTGA TTGCTTTTGT TGTTCCTATG GCTCAATACT  840

ATGCATATGT TTCAAAGAAG TGAACTGTCT GATTCTGGAA AGTTACATTT TCGTGAGATT  900

TGAGTAAGCA TGTATATTAT CGTGTACAAA ATGGTCCATT CGGAAATGAC TGATTC      956

ATG AGA TAT TTA AAA AGG ATA AAT ATG AAG ATT TGG ACC TCC CCT        1001
Met Arg Tyr Leu Lys Arg Ile Asn Met Lys Ile Trp Thr Ser Pro
1               5                  10                  15

AAC ATA ACG GAT ACT GCC ATT TCT TTT TCA GAG ATG CTG ACG CCA        1046
Asn Ile Thr Asp Thr Ala Ile Ser Phe Ser Glu Met Leu Thr Pro
                20                  25                  30

ATA AGT ACA GAC GGC TTG ATG ACT GAG ATG GGG GAG AGT AGT GGT        1091
Ile Ser Thr Asp Gly Leu Met Thr Glu Met Gly Glu Ser Ser Gly
                35                  40                  45
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GCT TAT ATT ATT CGC ATT CCT TTT GGA CCA AGA GAG AAA TAT ATT      1136
Ala Tyr Ile Ile Arg Ile Pro Phe Gly Pro Arg Glu Lys Tyr Ile
                50                  55                  60

CCA AAA GAA CAG CTA TGG CCC TAT ATT CCC GAA TTT GTT GAT GGT      1181
Pro Lys Glu Gln Leu Trp Pro Tyr Ile Pro Glu Phe Val Asp Gly
                65                  70                  75

GCA CTT AAC CAT ATT ATT CAA ATG TCC AAA GTT CTT GGG GAG CAA      1226
Ala Leu Asn His Ile Ile Gln Met Ser Lys Val Leu Gly Glu Gln
                80                  85                  90

ATT GGT AGT GGC TAT CCT GTG TGG CCT GTT GCC ATA CAC GGA CAT      1271
Ile Gly Ser Gly Tyr Pro Val Trp Pro Val Ala Ile His Gly His
                95                  100                 105

TAT GCT GAT GCT GGC GAC TCA GCT GCT CTC CTG TCA GGT GCT TTA      1316
Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
                110                 115                 120

AAT GTA CCA ATG CTT TTC ACT GGT CAC TCA CTT GGT AGA GAT AAG      1361
Asn Val Pro Met Leu Phe Thr Gly His Ser Leu Gly Arg Asp Lys
                125                 130                 135

TTG GAG CAA CTG TTG CGA CAA GGT CGT TTG TCA AAG GAT GAA ATA      1406
Leu Glu Gln Leu Leu Arg Gln Gly Arg Leu Ser Lys Asp Glu Ile
                140                 145                 150

AAC TCA ACC TAC AAG ATA ATG CGG AGA ATA GAG GCT GAA GAA TTA      1451
Asn Ser Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu
                155                 160                 165
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ACT CTT GAT GCT TCC GAA ATT GTC ATC ACT AGT ACA AGA CAG GAG      1496
Thr Leu Asp Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu
                170                 175                 180

ATT GAC GAG CAA TGG CGT TTG TAT GAT GGG TTT GAT CCA ATA TTA      1541
Ile Asp Glu Gln Trp Arg Leu Tyr Asp Gly Phe Asp Pro Ile Leu
                185                 190                 195

GAG CGT AAG TTA CGT GCA AGG ATC AAG CGC AAT GTC AGC TGT TAT      1586
Glu Arg Lys Leu Arg Ala Arg Ile Lys Arg Asn Val Ser Cys Tyr
                200                 205                 210

GGC AGG TTT ATG CCT CGT ATG GCT GTA ATT CCT CCT GGG ATG GAG      1631
Gly Arg Phe Met Pro Arg Met Ala Val Ile Pro Pro Gly Met Glu
                215                 220                 225

TTC CAC CAT ATT GTG CCA CAT GAA GGT GAC ATG GAT GGA GAA ACA      1676
Phe His His Ile Val Pro His Glu Gly Asp Met Asp Gly Glu Thr
                230                 235                 240

GAA GGA AGT GAA GAT GGG AAG ACC CCG GAT CCA CCT ATT TGG GCA      1721
Glu Gly Ser Glu Asp Gly Lys Thr Pro Asp Pro Pro Ile Trp Ala
                245                 250                 255

GAG ATT ATG CGC TTC TTT TCT AAT CCA AGG AAG CCT ATG ATA CTC      1766
Glu Ile Met Arg Phe Phe Ser Asn Pro Arg Lys Pro Met Ile Leu
                260                 265                 270

GCA CTT GCT AGG CCT GAT CCC AAG AAG AAC CTC ACT ACT TTA GTG      1811
Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn Leu Thr Thr Leu Val
                275                 280                 285

AAA GCA TTT GGT GAA TGT CGT CCA TTG AGA GAG CTT GCT AAT CTT      1856
Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn Leu
                290                 295                 300
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ACT TTG ATA ATG GGT AAT CGA GAT AAT ATC GAC GAA ATG TCT AGC      1901
Thr Leu Ile Met Gly Asn Arg Asp Asn Ile Asp Glu Met Ser Ser
                305                 310                 315

ACC AAT TCT GCA CTT CTT CTT TCA ATC TTG AAA ATG ATA GAT AAG      1946
Thr Asn Ser Ala Leu Leu Leu Ser Ile Leu Lys Met Ile Asp Lys
                320                 325                 330

TAT GAT CTT TAT GGT CAA GTA GCT TAT CCT AAA CAC CAC AAG CAG      1991
Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys Gln
                335                 340                 345

TCA GAT GTT CCT GAT ATC TAC CGT CTT GCT GCA AAG ACT AAG GGT      2036
Ser Asp Val Pro Asp Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly
                350                 355                 360

GTT TTT ATT AAT CCA GCT TTT ATT GAG CCT TTT GGA CTG ACT TTG      2081
Val Phe Ile Asn Pro Ala Phe Ile Glu Pro Phe Gly Leu Thr Leu
                365                 370                 375

ATT GAG GCA GCA GCT TAT GGT CTC CCA ATG GTA GCC ACA AAA AAT      2126
Ile Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Lys Asn
                380                 385                 390

GGA GGA CCT GTT GAT ATA CAT AGG GTT CTT GAC AAT GGT CTC TTA      2171
Gly Gly Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Leu Leu
                395                 400                 405

GTG GAT CCC CAT GAT CAG CAG GCA ATT GCT GAT GCT CTT TTG AAG      2216
Val Asp Pro His Asp Gln Gln Ala Ile Ala Asp Ala Leu Leu Lys
                410                 415                 420

TTG GTT GCT GAT AAG CAA CTG TGG GCT AAA TGC AGG GCA AAT GGA      2261
Leu Val Ala Asp Lys Gln Leu Trp Ala Lys Cys Arg Ala Asn Gly
                425                 430                 435
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TTA AAA AAT ATC CAC CTT TTC TCA TGG CCC GAG CAC TGT AAA ACT      2306
Leu Lys Asn Ile His Leu Phe Ser Trp Pro Glu His Cys Lys Thr
            440                 445                 450

TAT CTA TCC CGG ATA GCT AGC TGC AAA CCA AGG CAA CCA CGC TGG      2351
Tyr Leu Ser Arg Ile Ala Ser Cys Lys Pro Arg Gln Pro Arg Trp
            455                 460                 465

CTG AGA TCC ATT GAT GAT GAT GAT GAA AAT TCA GAA ACA GAT TCA      2396
Leu Arg Ser Ile Asp Asp Asp Asp Glu Asn Ser Glu Thr Asp Ser
            470                 475                 480

CCT AGT GAT TCC TTG AGA GAT ATT CAT GAT ATA TCT CTG AAT TTG      2441
Pro Ser Asp Ser Leu Arg Asp Ile His Asp Ile Ser Leu Asn Leu
            485                 490                 495

AGA TTT TCA TTA GAT GGG GAA AAG AAT GAC AAT AAA GAA AAT GCT      2486
Arg Phe Ser Leu Asp Gly Glu Lys Asn Asp Asn Lys Glu Asn Ala
            500                 505                 510

GAT AAT ACA TTA GAC CCC GAA GTT CGA AGG AGC AAG TTA GAG AAT      2531
Asp Asn Thr Leu Asp Pro Glu Val Arg Arg Ser Lys Leu Glu Asn
            515                 520                 525

GCT GTT TTG TCC TTA TCT AAG GGT GCA CTG AAG AGC ACA TCA AAA      2576
Ala Val Leu Ser Leu Ser Lys Gly Ala Leu Lys Ser Thr Ser Lys
            530                 535                 540

TCT TGG TCG TCA GAC AAG GCA GAC CAA AAC CCT GGT GCT GGT AAA      2621
Ser Trp Ser Ser Asp Lys Ala Asp Gln Asn Pro Gly Ala Gly Lys
            545                 550                 555

TTC CCA GCG ATT AGG AGG AGG CGA CAT ATT TTT GTT ATT GCA GTG      2666
Phe Pro Ala Ile Arg Arg Arg Arg His Ile Phe Val Ile Ala Val
            560                 560                 565
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GAT TGT GAT GCT AGC TCA GGA CTC TCT GGA AGT GTG AAA AAG ATA      2711
Asp Cys Asp Ala Ser Ser Gly Leu Ser Gly Ser Val Lys Lys Ile
                570                 575                 580

TTT GAG GCT GTA GAG AAG GAA AGG GCA GAG GGT TCC ATT GGA TTT      2756
Phe Glu Ala Val Glu Lys Glu Arg Ala Glu Gly Ser Ile Gly Phe
                585                 590                 595

ATC CTG GCT ACA TCT TTC AAT ATA TCA GAA GTA CAG TCT TTC CTG      2801
Ile Leu Ala Thr Ser Phe Asn Ile Ser Glu Val Gln Ser Phe Leu
                600                 605                 610

CTT TCA GAG GGC ATG AAT CCT ACT GAT TTT GAT GCT TAC ATA TGC      2846
Leu Ser Glu Gly Met Asn Pro Thr Asp Phe Asp Ala Tyr Ile Cys
                615                 620                 625

AAT AGT GGT GGT GAT CTT TAT TAT TCG TCC TTC CAT TCT GAG CAA      2891
Asn Ser Gly Gly Asp Leu Tyr Tyr Ser Ser Phe His Ser Glu Gln
                630                 635                 640

AAT CCT TTT GTA GTT GAC TTG TAC TAT CAC TCA CAT ATT GAG TAT      2936
Asn Pro Phe Val Val Asp Leu Tyr Tyr His Ser His Ile Glu Tyr
                645                 650                 655

CGT TGG GGG GGC GAA GGA TTG AGA AAG ACT TTG GTG CGT TGG GCC      2981
Arg Trp Gly Gly Glu Gly Leu Arg Lys Thr Leu Val Arg Trp Ala
                660                 665                 670

GCC TCT ATC ATT GAT AAG AAT GGT GAA AAT GGA GAT CAC ATT GTT      3026
Ala Ser Ile Ile Asp Lys Asn Gly Glu Asn Gly Asp His Ile Val
                675                 680                 685

GTT GAG GAT GAA GAC AAT TCA GCT GAC TAC TGC TAT ACT TTC AAA      3071
Val Glu Asp Glu Asp Asn Ser Ala Asp Tyr Cys Tyr Thr Phe Lys
                690                 695                 700
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GTC TGC AAG CCT GGG ACG GTT CCT CCA TCT AAA GAG CTT AGA AAA       3116
Val Cys Lys Pro Gly Thr Val Pro Pro Ser Lys Glu Leu Arg Lys
                705                 710                 715

GTA ATG CGA ATT CAG GCA CTT CGT TGT CAC GCT GTT TAT TGT CAA       3161
Val Met Arg Ile Gln Ala Leu Arg Cys His Ala Val Tyr Cys Gln
                720                 725                 730

AAT GGG AGT AGG ATT AAT GTG ATC CCT GTA CTG GCA TCT CGG TCC       3206
Asn Gly Ser Arg Ile Asn Val Ile Pro Val Leu Ala Ser Arg Ser
                735                 740                 745

CAA GCA CTC AGG TAC TTA TAT CTG CGA TGG GGA ATG GAC TTG TCG       3251
Gln Ala Leu Arg Tyr Leu Tyr Leu Arg Trp Gly Met Asp Leu Ser
                750                 755                 760

AAG TTG GTG GTT TTC GTC GGA GAA AGT GGT GAT ACC GAT TAT GAA       3296
Lys Leu Val Val Phe Val Gly Glu Ser Gly Asp Thr Asp Tyr Glu
                765                 770                 775

GGA TTA ATC GGT GGT CTA CGC AAG GCT GTC ATA ATG AAA GGC CTC       3341
Gly Leu Ile Gly Gly Leu Arg Lys Ala Val Ile Met Lys Gly Leu
                780                 785                 790

TGC ACT AAT GCA AGC AGC TTA ATT CAC GGT AAT AGG AAT TAC CCG       3386
Cys Thr Asn Ala Ser Ser Leu Ile His Gly Asn Arg Asn Tyr Pro
                795                 800                 805

CTA TCT GAT GTT TTA CCA TTC GAC AGC CCT AAT GTC ATC CAA GCG       3431
Leu Ser Asp Val Leu Pro Phe Asp Ser Pro Asn Val Ile Gln Ala
                810                 815                 820

GAC GAG GAA TGT AGC AGC ACC GAA ATC CGT TGC TTA CTG GTG AAA       3476
Asp Glu Glu Cys Ser Ser Thr Glu Ile Arg Cys Leu Leu Val Lys
                825                 830                 835
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CTA GCG GTA CTC AAA GGA TAATACCCTT CCCCCTTTGA TTGTCAAAAA 3524
Leu Ala Val Leu Lys Gly
840

CCTATATGAG CTATAAGACT ATGCCATGAA AAGAATGGCC ATCCATTTGG CTTGTCTTTT 3584

GAAGCTGTTA ATACTTTTCA ACAGACTACA AAATGAGATG AGTCCTTTGA TCCTCTTTAA 3644

AGGACATAAA AGCTTTATGC AAGAACCAGT GCTGTAAAGT TATAGAATTT CTTTTGCTAT 3704

ATATGACATT CGACAGAACC TGTTCCGGTT CATCGA 3740

SPS 2 sequence (Seq. ID No. 2)

ATTTTTTTCT CTAAGTTCTC TCTCGCTGTC CTTATCATTT CACCACCTCC ATAAATCTAG 60

AAACATCTTT TCTACTCCGT TAATCTCTCT AGCACACGGC GGAGGAGTGC GGCGGAGGAG 120

ATG GCG GGA AAC GAT TGG ATT AAC AGT TAC TTA GAG GCG ATA CTG 165
Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu
1 5 10 15

GAT GTT GGA CCA GGG CTA GAT GAT AAG AAG TCA TCG TTG TTG TTG 210
Asp Val Gly Pro Gly Leu Asp Asp Lys Lys Ser Ser Leu Leu Leu
20 25 30

AGA GAA AGA GGG AGG TTT AGT CCG ACG AGG TAC TTT GTT GAG GAA 255
Arg Glu Arg Gly Arg Phe Ser Pro Thr Arg Tyr Phe Val Glu Glu
35 40 45

GTT ATT ACT GGA TTC GAT GAG ACT GAT TTG CAT CGT TCG TGG ATC 300
Val Ile Thr Gly Phe Asp Glu Thr Asp Leu His Arg Ser Trp Ile
50 55 60

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CGA GCA CAA GCT ACT CGG AGT CCG CAG AGA AGG AAT ACT AGG CTC       345
Arg Ala Gln Ala Thr Arg Ser Pro Gln Arg Arg Asn Thr Arg Leu
                65                  70                  75

GAG AAT ATG TGC TGG AGG ATT TGG AAT TTG GCT CGC CAG AAA AAG       390
Glu Asn Met Cys Trp Arg Ile Trp Asn Leu Ala Arg Gln Lys Lys
                80                  85                  90

CAG CTT GAG GGA GAG CAA GCT CAG TGG ATG GCA AAA CGC CGT CAA       435
Gln Leu Glu Gly Glu Gln Ala Gln Trp Met Ala Lys Arg Arg Gln
                95                  100                 105

GAA CGT GAA AGA GGT CGC AGA GAA GCA GTT GCT GAT ATG TCA GAG       480
Glu Arg Glu Arg Gly Arg Arg Glu Ala Val Ala Asp Met Ser Glu
                110                 115                 120

GAT CTA TCT GAG GGA GAG AAA GGA GAT ATA GTC GCT GAC ATG TCA       525
Asp Leu Ser Glu Gly Glu Lys Gly Asp Ile Val Ala Asp Met Ser
                125                 130                 135

TCT CAT GGT GAA AGT ACC AGA GGC CGA TTG CCT AGA ATC AGT TCT       570
Ser His Gly Glu Ser Thr Arg Gly Arg Leu Pro Arg Ile Ser Ser
                140                 145                 150

GTT GAG ACA ATG GAA GCA TGG GTC AGT CAG CAG AGA GGA AAG AAG       615
Val Glu Thr Met Glu Ala Trp Val Ser Gln Gln Arg Gly Lys Lys
                155                 160                 165

CTT TAT ATC GTG CTT ATA AGT TTA CAT GGT TTA ATT CGG GGT GAG       660
Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Ile Arg Gly Glu
                170                 175                 180

AAT ATG GAG CTT GGA CGG GAT TCT GAT ACT GGT GGT CAG GTG AAG       705
Asn Met Glu Leu Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys
                185                 190                 195
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TAT GTT GTT GAA CTT GCG AGG GCC TTA GGG TCG ATG CCA GGT GTA        750
Tyr Val Val Glu Leu Ala Arg Ala Leu Gly Ser Met Pro Gly Val
                200                 205                 210

TAT CGG GTT GAC TTG CTT ACT AGA CAA GTA TCT TCA CCA GAA GTA        795
Tyr Arg Val Asp Leu Leu Thr Arg Gln Val Ser Ser Pro Glu Val
                215                 220                 225

GAT TGG AGC TAT GGT GAG CCG ACA GAG ATG CTG ACG CCA ATA AGT        840
Asp Trp Ser Tyr Gly Glu Pro Thr Glu Met Leu Thr Pro Ile Ser
                230                 235                 240

ACA GAC GGC TTG ATG ACT GAG ATG GGG GAG AGT AGT GGT GCT TAT        885
Thr Asp Gly Leu Met Thr Glu Met Gly Glu Ser Ser Gly Ala Tyr
                245                 250                 255

ATT ATT CGC ATT CCT TTT GGA CCA AGA GAG AAA TAT ATT CCA AAA        930
Ile Ile Arg Ile Pro Phe Gly Pro Arg Glu Lys Tyr Ile Pro Lys
                260                 265                 270

GAA CAG CTA TGG CCC TAT ATT CCC GAA TTT GTT GAT GGT GCA CTT        975
Glu Gln Leu Trp Pro Tyr Ile Pro Glu Phe Val Asp Gly Ala Leu
                275                 280                 285

AAC CAT ATT ATT CAA ATG TCC AAA GTT CTT GGG GAG CAA ATT GGT       1020
Asn His Ile Ile Gln Met Ser Lys Val Leu Gly Glu Gln Ile Gly
                290                 295                 300

AGT GGC TAT CCT GTG TGG CCT GTT GCC ATA CAC GGA CAT TAT GCT       1065
Ser Gly Tyr Pro Val Trp Pro Val Ala Ile His Gly His Tyr Ala
                305                 310                 315

GAT GCT GGC GAC TCA GCT GCT CTC CTG TCA GGT GCT TTA AAT GTA       1110
Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu Asn Val
                320                 330                 335
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CCA ATG CTT TTC ACT GGT CAC TCA CTT GGT AGA GAT AAG TTG GAG      1155
Pro Met Leu Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu Glu
                340                 345                 350

CAA CTG TTG GCA CAA GGT CGA AAG TCA AAG GAT GAA ATA AAC TCA      1200
Gln Leu Leu Ala Gln Gly Arg Lys Ser Lys Asp Glu Ile Asn Ser
                355                 360                 365

ACC TAC AAG ATA ATG CGG AGA ATA GAG GCT GAA GAA TTA ACT CTT      1245
Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Thr Leu
                370                 375                 380

GAT GCT TCC GAA ATT GTC ATC ACT AGT ACA AGA CAG GAG ATT GAC      1290
Asp Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Asp
                385                 390                 395

GAG CAA TGG CGT TTG TAT GAT GGG TTT GAT CCA ATA TTA GAG CGT      1335
Glu Gln Trp Arg Leu Tyr Asp Gly Phe Asp Pro Ile Leu Glu Arg
                400                 405                 410

AAG TTA CGT GCA AGG ATC AAG CGC AAT GTC AGC TGT TAT GGC AGG      1380
Lys Leu Arg Ala Arg Ile Lys Arg Asn Val Ser Cys Tyr Gly Arg
                415                 420                 425

TTT ATG CCT CGT ATG GCT GTA ATT CCT CCT GGG ATG GAG TTC CAC      1425
Phe Met Pro Arg Met Ala Val Ile Pro Pro Gly Met Glu Phe His
                430                 435                 440

CAT ATT GTG CCA CAT GAA GGT GAC ATG GAT GGT GAA ACA GAA GGA      1470
His Ile Val Pro His Glu Gly Asp Met Asp Gly Glu Thr Glu Gly
                445                 450                 455

AGT GAA GAT GGG AAG ACC CCG GAT CCA CCT ATT TGG GCA GAG ATT      1515
Ser Glu Asp Gly Lys Thr Pro Asp Pro Pro Ile Trp Ala Glu Ile
                460                 465                 470
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ATG CGC TTC TTT TCT AAT CCA AGG AAG CCT ATG ATA CTC GCA CTT      1560
Met Arg Phe Phe Ser Asn Pro Arg Lys Pro Met Ile Leu Ala Leu
                475                 480                 485

GCT AGG CCT GAT CCC AAG AAG AAC CTC ACT ACT TTA GTG AAA GCA      1605
Ala Arg Pro Asp Pro Lys Lys Asn Leu Thr Thr Leu Val Lys Ala
                490                 495                 500

TTT GGT GAA TGT CGT CCA TTG AGA GAG CTT GCT AAT CTT ACT TTG      1650
Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn Leu Thr Leu
                505                 510                 515

ATA ATG GGT AAT CGA GAT AAT ATC GAC GAA ATG TCT AGC ACC AAT      1695
Ile Met Gly Asn Arg Asp Asn Ile Asp Glu Met Ser Ser Thr Asn
                520                 525                 530

TCT GCA CTT CTT CTT TCA ATC TTG AAA ATG ATA GAT AAG TAT GAT      1740
Ser Ala Leu Leu Leu Ser Ile Leu Lys Met Ile Asp Lys Tyr Asp
                535                 540                 540

CTT TAT GGT CAA GTA GCT TAT CCT AAA CAC CAC AAG CAG TCA GAT      1785
Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys Gln Ser Asp
                545                 550                 555

GTT CCT GAT ATC TAC CGT CTT GCT GCA AAG ACT AAG GGT GTT TTT      1830
Val Pro Asp Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly Val Phe
                560                 565                 570

ATT AAT CCA GCT TTT ATT GAG CCT TTT GGA CTG ACT TTG ATT GAG      1875
Ile Asn Pro Ala Phe Ile Glu Pro Phe Gly Leu Thr Leu Ile Glu
                575                 580                 585

GCA GCA GCT TAT GGT CTC CCA ATG GTA GCC ACA AAA AAT GGA GGA      1920
Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Lys Asn Gly Gly
                590                 595                 600
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CCT GTT GAT ATA CAT AGG GTT CTT GAC AAT GGT CTC TTA GTG GAT      1965
Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Leu Leu Val Asp
                605                 610                 615

CCC CAT GAT CAG CAG GCA ATT GCT GAT GCT CTT TTG AAG TTG GTT      2010
Pro His Asp Gln Gln Ala Ile Ala Asp Ala Leu Leu Lys Leu Val
                620                 625                 630

GCT GAT AAG CAA CTG TGG GCT AAA TGC AGG GCA AAT GGA TTA AAA      2055
Ala Asp Lys Gln Leu Trp Ala Lys Cys Arg Ala Asn Gly Leu Lys
                635                 640                 645

AAT ATC CAC CTT TTC TCA TGG CCC GAG CAC TGT AAA ACT TAT CTA      2100
Asn Ile His Leu Phe Ser Trp Pro Glu His Cys Lys Thr Tyr Leu
                650                 655                 660

TCC CGG ATA GCT AGC TGC AAA CCA AGG CAA CCA CGC TGG CTG AGA      2145
Ser Arg Ile Ala Ser Cys Lys Pro Arg Gln Pro Arg Trp Leu Arg
                665                 670                 675

TCC ATT GAT GAT GAT GAT GAA AAT TCA GAA ACA GAT TCA CCT AGT      2190
Ser Ile Asp Asp Asp Asp Glu Asn Ser Glu Thr Asp Ser Pro Ser
                680                 685                 690

GAT TCC TTG AGA GAT ATT CAT GAT ATA TCT CTG AAT TTG AGA TTT      2235
Asp Ser Leu Arg Asp Ile His Asp Ile Ser Leu Asn Leu Arg Phe
                695                 700                 705

TCA TTA GAT GGG GAA AAG AAT GAC AAT AAA GAA AAT GCT GAT AAT      2280
Ser Leu Asp Gly Glu Lys Asn Asp Asn Lys Glu Asn Ala Asp Asn
                710                 715                 720

ACA TTA GAC CCC GAA GTT CGA AGG AGC AAG TTA GAG AAT GCT GTT      2325
Thr Leu Asp Pro Glu Val Arg Arg Ser Lys Leu Glu Asn Ala Val
                725                 730                 735
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TTG TCC TTA TCT AAG GGT GCA CTG AAG AGC ACA TCA AAA TCT TGG      2370
Leu Ser Leu Ser Lys Gly Ala Leu Lys Ser Thr Ser Lys Ser Trp
                740                 745                 750

TCG TCA GAC AAG GCA GAC CAA AAC CCT GGT GCT GGT AAA TTC CCA      2415
Ser Ser Asp Lys Ala Asp Gln Asn Pro Gly Ala Gly Lys Phe Pro
                755                 760                 765

GCG ATT AGG AGG AGG CGA CAT ATT TTT GTT ATT GCA GTG GAT TGT      2460
Ala Ile Arg Arg Arg Arg His Ile Phe Val Ile Ala Val Asp Cys
                770                 775                 780

GAT GCT AGC TCA GGA CTC TCT GGA AGT GTG AAA AAG ATA TTT GAG      2505
Asp Ala Ser Ser Gly Leu Ser Gly Ser Val Lys Lys Ile Phe Glu
                785                 790                 795

GCT GTA GAG AAG GAA AGG GCA GAG GGT TCC ATT GGA TTT ATC CTG      2550
Ala Val Glu Lys Glu Arg Ala Glu Gly Ser Ile Gly Phe Ile Leu
                800                 805                 810

GCT ACA TCT TTC AAT ATA TCA GAA GTA CAG TCT TTC CTG CTT TCA      2595
Ala Thr Ser Phe Asn Ile Ser Glu Val Gln Ser Phe Leu Leu Ser
                815                 820                 825

GAG GGC ATG AAT CCT ACT GAT TTT GAT GCT TAC ATA TGC AAT AGT      2640
Glu Gly Met Asn Pro Thr Asp Phe Asp Ala Tyr Ile Cys Asn Ser
                830                 835                 840

GGT GGT GAT CTT TAT TAT TCG TCC TTC CAT TCT GAG CAA AAT CCT      2685
Gly Gly Asp Leu Tyr Tyr Ser Ser Phe His Ser Glu Gln Asn Pro
                845                 850                 855

TTT GTA GTT GAC TTG TAC TAT CAC TCA CAT ATT GAG TAT CGT TGG      2730
Phe Val Val Asp Leu Tyr Tyr His Ser His Ile Glu Tyr Arg Trp
                860                 865                 870
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GGG GGC GAA GGA TTG AGA AAG ACT TTG GTG CGT TGG GCC GCC TCT      2775
Gly Gly Glu Gly Leu Arg Lys Thr Leu Val Arg Trp Ala Ala Ser
                875                 880                 885

ATC ATT GAT AAG AAT GGT GAA AAT GGA GAT CAC ATT GTT GTT GAG      2820
Ile Ile Asp Lys Asn Gly Glu Asn Gly Asp His Ile Val Val Glu
                890                 895                 900

GAT GAA GAC AAT TCA GCT GAC TAC TGC TAT ACT TTC AAA GTC TGC      2865
Asp Glu Asp Asn Ser Ala Asp Tyr Cys Tyr Thr Phe Lys Val Cys
                905                 910                 915

AAG CCT GGG ACG GTT CCT CCA TCT AAA GAG CTT AGA AAA GTA ATG      2910
Lys Pro Gly Thr Val Pro Pro Ser Lys Glu Leu Arg Lys Val Met
                920                 925                 930

CGA ATT CAG GCA CTT CGT TGT CAC GCT GTT TAT TGT CAA AAT GGG      2955
Arg Ile Gln Ala Leu Arg Cys His Ala Val Tyr Cys Gln Asn Gly
                935                 940                 945

AGT AGG ATT AAT GTG ATC CCT GTA CTG GCA TCT CGG TCC CAA GCA      3000
Ser Arg Ile Asn Val Ile Pro Val Leu Ala Ser Arg Ser Gln Ala
                950                 955                 960

CTC AGG TAC TTA TAT CTG CGA TGG GGA ATG GAC TTG TCG AAG TTG      3045
Leu Arg Tyr Leu Tyr Leu Arg Trp Gly Met Asp Leu Ser Lys Leu
                965                 970                 975

GTG GTT TTC GTC GGA GAA AGT GGT GAT ACC GAT TAT GAA GGA TTA      3090
Val Val Phe Val Gly Glu Ser Gly Asp Thr Asp Tyr Glu Gly Leu
                980                 985                 990

ATC GGT GGT CTA CGC AAG GCT GTC ATA ATG AAA GGC CTC TGC ACT      3135
Ile Gly Gly Leu Arg Lys Ala Val Ile Met Lys Gly Leu Cys Thr
                995                1000                1005
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AAT GCA AGC AGC TTA ATT CAC GGT AAT AGG AAT TAC CCG CTA TCT      3180
Asn Ala Ser Ser Leu Ile His Gly Asn Arg Asn Tyr Pro Leu Ser
                1010                1015                1020

GAT GTT TTA CCA TTC GAC AGC CCT AAT GTC ATC CAA GCG GAC GAG      3225
Asp Val Leu Pro Phe Asp Ser Pro Asn Val Ile Gln Ala Asp Glu
                1025                1030                1035

GAA TGT AGC AGC ACC GAA ATC CGT TGC TTA CTG GAG AAA CTA GCG      3270
Glu Cys Ser Ser Thr Glu Ile Arg Cys Leu Leu Glu Lys Leu Ala
                1040                1045                1050

GTA CTC AAA GGA TAA TACCCTTCCC CCTTTGATTG TCAAAAACCT            3315
Val Leu Lys Gly End
            1054

ATATGAGCTA TAAGACTATG CCATGAAAAG AATGGCCATC CATTTGGCTT GTCTTTTGAA 3375

GCTGTTAATA CTTTTCAACA GACTACAAAA TGAGATGAGT CCTTTGATCC TCTTTAAAGG 3435

ACATAAAAGC TTTATGCAAG AACCAGTGCT GTAAAGTTAT AGAATTTCTT TTGCTATATA 3495

TGACATTCGA CAGAACCAGT TCCGGTTCAT CGAGAAAAAG AAATAAATTT CAACTTATAA 3555

ACATGCCTGA TCATGTAAAT TATCATATAC ATCCATCGGA AGGCATTATC GATGGGTTAT 3615

CAGATTTTTT  3625
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SPS 3 sequence (Seq. ID No.3)

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ATTTTTT TCTCTAAATT CTCTCTCACT GTCCTTATCA TTTCACCACC TCCATAAATC  57

TAGAAACATC TTTTCTATTC CGTTAATCTC TCTAGCACAC GGCGGAGTGC GGCGGAGGAG 117
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ATG GCG GGA AAC GAC TGG ATT AAC AGT TAC TTA GAG GCG ATA CTG        162
Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu
1               5                   10                  15

GAT GTA GGA CCA GGG CTA GAT GAT AAG AAA TCA TCG TTG TTG TTG        207
Asp Val Gly Pro Gly Leu Asp Asp Lys Lys Ser Ser Leu Leu Leu
                20                  25                  30

AGA GAA AGA GGG AGG TTT AGT CCG ACG AGG TAC TTT GTT GAG GAA        252
Arg Glu Arg Gly Arg Phe Ser Pro Thr Arg Tyr Phe Val Glu Glu
                35                  40                  45

GTT ATT ACT GGA TTC GAT GAG ACT GAT TTG CAT CGC TCG TGG ATC        297
Val Ile Thr Gly Phe Asp Glu Thr Asp Leu His Arg Ser Trp Ile
                50                  55                  60

CGA GCA CAA GCT ACT CGG AGT CCG CAG GAG AGG AAT ACT AGG CTC        342
Arg Ala Gln Ala Thr Arg Ser Pro Gln Glu Arg Asn Thr Arg Leu
                65                  70                  75

GAG AAT ATG TGC TGG AGG ATT TGG AAT TTG GCT CGC CAG AAA AAG        387
Glu Asn Met Cys Trp Arg Ile Trp Asn Leu Ala Arg Gln Lys Lys
                80                  85                  90

CAG CTT GAG GGA GAG CAA GCT CAG TGG ATG GCA AAA CGC CGT CAA        432
Gln Leu Glu Gly Glu Gln Ala Gln Trp Met Ala Lys Arg Arg Gln
                95                  100                 105

GAA CGT GAG AGA GGT CGC AGA GAA GCA GTT GCT GAT ATG TCA GAG        477
Glu Arg Glu Arg Gly Arg Arg Glu Ala Val Ala Asp Met Ser Glu
                110                 115                 120

GAT CTA TCT GAG GGA GAG AAA GGA GAT ATA GTC GCT GAC ATG TCA        522
Asp Leu Ser Glu Gly Glu Lys Gly Asp Ile Val Ala Asp Met Ser
                125                 130                 135
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TCT CAT GGT GAA AGT ACC AGA GGC CGA TTG CCT AGA ATC AGT TCT      567
Ser His Gly Glu Ser Thr Arg Gly Arg Leu Pro Arg Ile Ser Ser
                140                 145                 150

GTT GAG ACA ATG GAA GCA TGG GTC AGT CAG CAG AGA GGA AAG AAG      612
Val Glu Thr Met Glu Ala Trp Val Ser Gln Gln Arg Gly Lys Lys
                155                 160                 165

CTT TAT ATC GTG CTT ATA AGT TTA CAT GGT TTA ATT CGG GGT GAG      657
Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Ile Arg Gly Glu
                170                 175                 180

AAT ATG GAG CTT GGA CGG GAT TCT GAT ACT GGT GGT CAG GTG AAG      702
Asn Met Glu Leu Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys
                185                 190                 195

TAT GTA GTT GGA GCA ACT GTT GCA CAA GGT CGT TTG TCA AAG GAT      747
Tyr Val Val Gly Ala Thr Val Ala Gln Gly Arg Leu Ser Lys Asp
                200                 205                 210

GAA ATA AAC TCA ACC TAC AAG ATA ATG CGG AGA ATA GAG GCT GAA      792
Glu Ile Asn Ser Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu
                215                 220                 225

GAA TTA ACT CTT GAT GCT TCC GAA ATT GTC ATC ACT AGT ACA AGA      837
Glu Leu Thr Leu Asp Ala Ser Glu Ile Val Ile Thr Ser Thr Arg
                230                 235                 240

CAG GAG ATT GAC GAG CAA TGG CGT TTG TAT GAT GGG TTT GAT CCA      882
Gln Glu Ile Asp Glu Gln Trp Arg Leu Tyr Asp Gly Phe Asp Pro
                245                 250                 255

ATA TTA GAG CGT AAG TTA CGT GCA AGG ATC AAG CGC AAT GTC AGC      927
Ile Leu Glu Arg Lys Leu Arg Ala Arg Ile Lys Arg Asn Val Ser
                260                 265                 270
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TGT TAT GGC AGG TTT ATG CCT CGT ATG GCT GTA ATT CCT CCT GGG      972
Cys Tyr Gly Arg Phe Met Pro Arg Met Ala Val Ile Pro Pro Gly
                275                 280                 285

ATG GAG TTC CAC CAT ATT GTG CCA CAT GAA GGT GAC ATG GAT GGT     1017
Met Glu Phe His His Ile Val Pro His Glu Gly Asp Met Asp Gly
                290                 295                 300

GAA ACA GAA GGA AGT GAA GAT GGA AAG ACC CCG GAT CCA CCT ATT     1062
Glu Thr Glu Gly Ser Glu Asp Gly Lys Thr Pro Asp Pro Pro Ile
                305                 310                 315

TGG GCA GAG ATT ATG CGC TTC TTT TCT AAT CCA AGG AAG CCT ATG     1107
Trp Ala Glu Ile Met Arg Phe Phe Ser Asn Pro Arg Lys Pro Met
                320                 330                 335

ATA CTC GCA CTT GCT AGG CCT GAT CCC AAG AAG AAC CTC ACT ACT     1152
Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn Leu Thr Thr
                340                 345                 350

TTA GTG AAA GCA TTT GGT GAA TGT CGT CCA TTG AGA GAC CTT GCT     1197
Leu Val Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Asp Leu Ala
                355                 360                 365

AAT CTT ACT TTG ATA ATG GGT AAT CGA GAT AAT ATC GAC GAA ATG     1242
Asn Leu Thr Leu Ile Met Gly Asn Arg Asp Asn Ile Asp Glu Met
                370                 375                 380

TCT AGC ACC AAT TCT GCA CTT CTT CTT TCA ATC TTG AAG ATG ATA     1287
Ser Ser Thr Asn Ser Ala Leu Leu Leu Ser Ile Leu Lys Met Ile
                385                 390                 395

GAT AAG TAT GAT CTT TAT GGT CTA GTA GCT TAT CCT AAA CAC CAC     1332
Asp Lys Tyr Asp Leu Tyr Gly Leu Val Ala Tyr Pro Lys His His
                400                 405                 410
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AAG CAG TCA GAT GTT CCT GAT ATC TAC CGT CTT GCT GCA AAG ACT      1377
Lys Gln Ser Asp Val Pro Asp Ile Tyr Arg Leu Ala Ala Lys Thr
                415                 420                 425

AAG GGT GTT TTT ATT AAT CCA GCT TTT ATT GAG CCT TTT GGA CTG      1422
Lys Gly Val Phe Ile Asn Pro Ala Phe Ile Glu Pro Phe Gly Leu
                430                 435                 440

ACT TTG ATT GAG GCA GCA GCT TAT GGT CTC CCA ATG GTA GCC ACA      1467
Thr Leu Ile Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr
                445                 450                 455

AAA AAT GGA GGA CCT GTT GAT ATA CAT AGG GTT CTT GAC AAT GGT      1512
Lys Asn Gly Gly Pro Val Asp Ile His Arg Val Leu Asp Asn Gly
                460                 465                 470

CTC TTA GTG GAT CCC CAT GAT CAG CAG GCA ATT GCT GAT GCT CTT      1557
Leu Leu Val Asp Pro His Asp Gln Gln Ala Ile Ala Asp Ala Leu
                475                 480                 485

TTG AAG TTG GTT GCT GAT AAG CAA CTG TGG GCT AAA TGC AGG GCA      1602
Leu Lys Leu Val Ala Asp Lys Gln Leu Trp Ala Lys Cys Arg Ala
                490                 495                 500

AAT GGA TTA AAA AAT ATC CAC CTT TTC TCA TGG CCC GAG CAC TGT      1647
Asn Gly Leu Lys Asn Ile His Leu Phe Ser Trp Pro Glu His Cys
                505                 510                 515

AAA ACT TAT CTA TCC CGG ATA GCT AGC TGC AAA CCG AGG CAA CAT      1692
Lys Thr Tyr Leu Ser Arg Ile Ala Ser Cys Lys Pro Arg Gln His
                520                 525                 530

TCC TTG AGA GAT ATT CAT GAT ATA TCT CTG AAT TTG AGA TTT TCA      1737
Ser Leu Arg Asp Ile His Asp Ile Ser Leu Asn Leu Arg Phe Ser
                535                 540                 540
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TTA GAT GGG GAA AAG AAT GAC AAT AAA GAA AAT GCT GAT AAT ACA      1782
Leu Asp Gly Glu Lys Asn Asp Asn Lys Glu Asn Ala Asp Asn Thr
                545                 550                 555

TTA GAC CCC GAA GTT CGA AGG AGC AAG TTA GAG AAT GCT GTT TTG      1827
Leu Asp Pro Glu Val Arg Arg Ser Lys Leu Glu Asn Ala Val Leu
                560                 565                 570

TCC TTA TCT AAG GGT GCA CTG AAG AGC ACA TCA AAA TCT TGG TCG      1872
Ser Leu Ser Lys Gly Ala Leu Lys Ser Thr Ser Lys Ser Trp Ser
                575                 580                 585

TCA GAC AAG GCA GAC CAA AAT CCT GGT GCT GGT AAA TTC CCA GCG      1917
Ser Asp Lys Ala Asp Gln Asn Pro Gly Ala Gly Lys Phe Pro Ala
                590                 595                 600

ATT AGG AGG AGG CGA CAT ATT TTT GTT ATT GCA GTG GAT TGT GAT      1962
Ile Arg Arg Arg Arg His Ile Phe Val Ile Ala Val Asp Cys Asp
                605                 610                 615

GCT AGC TCA GGA CTC TCT GGA AGT ATG AAA AAG ATA TTT GAG GCT      2007
Ala Ser Ser Gly Leu Ser Gly Ser Met Lys Lys Ile Phe Glu Ala
                620                 625                 630

GTA GAG AAG GAA AGG GCA GAG GGT TCC ATT GGA TTT ATC CTT GCT      2052
Val Glu Lys Glu Arg Ala Glu Gly Ser Ile Gly Phe Ile Leu Ala
                635                 640                 645

ACA TCT TTC AAT ATA TCA GAA GTA CAG TCT TTC CTG CTT TCA GAG      2097
Thr Ser Phe Asn Ile Ser Glu Val Gln Ser Phe Leu Leu Ser Glu
                650                 655                 660

GGC ATG AAT CCT ACT GAG CAA AAT CCT TTT GTA GTT GAC TTG TAC      2142
Gly Met Asn Pro Thr Glu Gln Asn Pro Phe Val Val Asp Leu Tyr
                665                 670                 675
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TAT CAC TCA CAT ATT GAG TAT CGT TGG GGG GGC GAA GGG TTG AGA      2187
Tyr His Ser His Ile Glu Tyr Arg Trp Gly Gly Glu Gly Leu Arg
                680                 685                 690

AAG ACT TTG GTG CGT TGG GCC GCC TCT ATC ATT GAT AAG AAT GGT      2232
Lys Thr Leu Val Arg Trp Ala Ala Ser Ile Ile Asp Lys Asn Gly
                695                 700                 705

GAA AAT GGA GAT CAC ATT GTT GTT GAG GAT GAA GAC AAT TCA GCT      2277
Glu Asn Gly Asp His Ile Val Val Glu Asp Glu Asp Asn Ser Ala
                710                 715                 720

GAC TAC TGC TAT ACA TTC AAA GTT TGC AAG CCT GGG ACG GTT CCT      2322
Asp Tyr Cys Tyr Thr Phe Lys Val Cys Lys Pro Gly Thr Val Pro
                725                 730                 735

CCA TCT AAA GAA CTT AGA AAA GTA ATG CGA ATT CAG GCA CTT CGT      2367
Pro Ser Lys Glu Leu Arg Lys Val Met Arg Ile Gln Ala Leu Arg
                740                 745                 750

TGT CAC GCT GTT TAT TGT CAA AAT GGG AGT AGG ATT AAT GTG ATC      2412
Cys His Ala Val Tyr Cys Gln Asn Gly Ser Arg Ile Asn Val Ile
                755                 760                 765

CCT GTA CTG GCA TCT CGG TCC CAA GCA CTC AGG TAC TTA TAT CTG      2457
Pro Val Leu Ala Ser Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Leu
                770                 775                 780

CGA TGG GGA ATG GTC CCT GTA CTG GCA TCT CGG TCC CAA GCA CTC      2502
Arg Trp Gly Met Val Pro Val Leu Ala Ser Arg Ser Gln Ala Leu
                785                 790                 795

AGG TAC TTA TAT CTG CGA TGG GGA ATG GTC CCT GTA CTG GCA TCT      2547
Arg Tyr Leu Tyr Leu Arg Trp Gly Met Val Pro Val Leu Ala Ser
                800                 805                 810
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CGG TCC CAA GCA CTC AGG TAC TTA TAT CTG CGA TGG GGA ATG GAC      2592
Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Leu Arg Trp Gly Met Asp
                815                 820                 825

TTG TCG AAG TTG GTG GTT TTC GTC GGA GAA AGT GGT GAT ACC GAT      2637
Leu Ser Lys Leu Val Val Phe Val Gly Glu Ser Gly Asp Thr Asp
                830                 835                 840

TAT GAA GGA TTG ATC GGT GGT CTA CGC AAG GCT GTC ATA ATG AAA      2682
Tyr Glu Gly Leu Ile Gly Gly Leu Arg Lys Ala Val Ile Met Lys
                845                 850                 855

GGA CTC TGC ACT AAT GCA AGC AGC TTA ATT CAC GGT AAT AGG AAT      2727
Gly Leu Cys Thr Asn Ala Ser Ser Leu Ile His Gly Asn Arg Asn
                860                 865                 870

TAC CCG CTA TCT GAT GTT TTA CCA TTC GAG AGC CCT AAT GTC ATC      2772
Tyr Pro Leu Ser Asp Val Leu Pro Phe Glu Ser Pro Asn Val Ile
                875                 880                 885

CAA GCG GAT GAG GAA TGT AGC AGC ACC GGA ATC CGT TCC TTA CTG      2817
Gln Ala Asp Glu Glu Cys Ser Ser Thr Gly Ile Arg Ser Leu Leu
                905                 910                 915

GAG AAA CTA GCG GTA CTC AAA GGA TAA TACCCTTCCC CCTTTGATTG        2864
Glu Lys Leu Ala Val Leu Lys Gly End
                920

TCAAAAACCT ATATGAGCTA AGATTATGCC ATGAAAAGAA TGGCCATCCA TTTGGCTTGT2924

CTTTTG  2930
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All sequences are cDNA sequences and stem from a cDNA libaray of leaf tissue. The expression gene is the same in various plant tissues. As promoter, there can generally be used any promoter which is active in plants. The promoter should ensure that the foreign gene is expressed in the plant. The promoter can be so chosen that the expression occurs only in specified tissues, at a determined time point in the plant's development or at a time point determined by outside influences. The promoter can be homologous or heterologous to the plant. Suitable promoters are e.g. the promoter of the 35S RNA of the cauliflower mosaic virus, the patatin promoter B33 (Rocha-Sosa et al. (1989) EMBO J 8: 23-29) or a promoter that ensures an expression only in photosynthetically active tissues. Other promoters can be used which ensure an expression only in specified organs, such as the root, tuber, seed, stem or specified cell types such as mesophyllic, epidermal or transport cells. For hindering cold sweetening, suitable promoters are those which ensure an activation of the transcription is stored in harvested parts of the plants. For this, there can be considered cold induced promoters or such promoters, that become active during the transition of the tuber from the phase where it stores material to the phase where it gives up material.

The coding sequence contains the information for the formation of an mRNA for the sucrose-phosphate-synthase or for the formation of an anti-sense RNA for the SPS. whether the translatable mRNA or an anti-sense RNA is formed, depends on the orientation of the coding sequence in relation to the promoter. If the 3′ end of the coding sequence is fused to the 3′ end of the promoter, an anti-sense RNA results, and by fusion of the 5′ end of the coding to the 3′ end of the promoter a translatable RNA

results. This latter leads to an increase of the SPS activity in the cell, whilst the first leads to a reduction of the SPS activity in the cell. Such a reduction of SPS activity is of especial significance in view of the undesirable formation of sucrose and/or reducing sugars as a result of cold storage of harvested organs.

The coding sequence for SPS can be one of the three described above or one that is derived by modifications of the sequences described above. A derivation can be carried out, e.g. by current methods of mutagenesis and/or recombination. For this especially, changes of SPS sequences are envisaged, that lead to a neutralisation of the plant's own regulation mechanism.

The DNA sequences of the invention can be used for the preparation of derivatives whose gene products are not subjected to the plant's own activity regulation during a phosphorylation reaction.

Further, the sequences can also be used for the preparation of derivatives by targeted and non-targeted mutagenesis.

The invention relates further to derivatives of the DNA sequences of the invention that are obtained by exchange of single bases or by deletion or insertion of base sequences and which code for proteins with a comparable activity to sucrose-phosphate-synthase.

The 5' untranslated area of the sequence Seq. ID No 1 definitely does not belong to SPS, but is added as a cloning artefact. The methionine start codon of the coding region lies in a region in which no homology of the amino

acid sequence to the other SPS sequences is involved. Since this sequence does not also fully coincide in the homologous region with one of the other sequences, it is recognisable that the sequence Seq. ID No 1 is not a derivative of the sequences Seq. ID No 2 and Seq. ID No 3.

The termination sequence provides the correct finishing of the transcription and the attachment of a polyadenyl group to the RNA. This polyadenyl group has an important function in the stabilisation of RNA molecules in the cells. With suitable plasmids, which contain the DNA sequences of the invention, plants can be transformed with the object of raising and/or reducing the SPS activity and/or the modification of the sucrose concentration.

Plasmids, that can be used are e.g. p35S-anti-pot-SPS (DSM 7125) and pB33-anti-pot-SPS (DSM 7124). With the gene 35S-anti-pot-SPS, located on the plasmid p35S-anti-pot-SPS, the concentration of the mRNA for the SPS protein and the enzymatic activity, for example, can be reduced. With the gene B33S-anti-pot-SPS, located on the plasmid pB33-anti-pot-SPS, the concentration of the mRNA for the SPS protein and the enzymatic activity, specifically for potato tubers for example, can be reduced. In a similar way to the SPS sequence (Seq. ID No. 1) located on this plasmid, other SPS sequences, e.g. the sequences Seq. ID No. 2 and Seq. ID No. 3 also be cloned in suitable vectors and for the same purpose.

In the plant, the SPS is subjected to an activity control by phosphorylation. This allows the plant to regulate the activity of the enzyme within a fixed frame independent of the amount of the SPS protein. If one of the changes occurring outside the activity of the SPS is to achieved, it is necessary to evade the plant's own regulation

mechanism. Therefore changing the phosphorylation possibilities is an important target for influencing the SPS activity and thus the sucrose content of the plant.

It is not known, in which position in the SPS protein, target directed changes of the coding regions can be achieved, which serve the purpose of introducing in the plant, SPS activity, which is not subject to any of the plant's own controls.

The DNA sequence described here, which contains the coding region for SPS from *Solanum tuberosum*, allows the identification of the sites of protein phosphorylation of the SPS. By using standard methods (Sambrook, J., Fritsch, E. F., Maniatis, T. (1989) Molecular Cloning: A laboratory Manual, 2nd. Edn., Cold Spring Harbor Laboratory Press, NY, USA), a localisation of the phosphorylation positions of SPS is possible using the DNA sequences of the invention. These being known, by use of the plasmids with the SPS sequence, a target directed mutagenesis (Sambrook et al, 1989) of the coding region of SPS and/or a non-target directed mutagenesis (Sambrook et al, 1989) and subsequent probing of the desired mutations of the coding region of the SPS can be undertaken. Derivatives of the coding region can be prepared with the help of this plasmid, whose derived proteins are not subjected to the plants own regulation mechanisms.

Since the SPS enzyme is regulated by phosphorylation in all tested species, except maize, one can refer to sequence comparisons, to identify possible phosphorylation sites. The criterium for this is that a serine residue appears in an acidic medium in the regulated SPS protein, but not however with maize.

There are 12 such serine residues in the sequences Seq. ID No. 2 and Seq ID No. 3. In the sequence Seq ID No. 1, the first of the 12 serine residues is missing, since the coding region begins just later. The sequence Seq. ID No. 1 is thus especially suitable for the production of an SPS activity in plants, that is not liable to endogenous activity regulation.

For the introduction of the SPS sequence in higher plants, a large number of cloning vectors are available, which contain a replication signal for *E. coli* and a marker, which allows a selection of the transformed cells. Examples of vectors are pBR 322, pUC-series, M13 mp-series, pACYC 184; EMBL 3 etc.. According to the introduction method of the desired gene in the plant, other DNA sequences may be suitable. Should the Ti- or Ri-plasmid be used, e.g. for the transformation of the plant cell, then at least the right boundary, often however both the right and left boundary of the Ti- and Ri-Plasmid T-DNA, is attached, as a flanking region, to the gene being introduced. The use of T-DNA for the transformation of plants cells has been intensively researched and is well described in EP 120 516; Hoekama, In: The Binary Plant Vector System, Offset-drukkerij Kanters B.V. Alblasserdam, (1985), Chapter V; Fraley, et al., Crit. Rev. Plant Sci., 4:1-46 and An et al. (1985) EMBO J. 4: 277-287. Once the introduced DNA is integrated in the genome, it is as a rule stable there and remains also in the offspring of the original transformed cells. It normally contains a selection marker, which induces resistance in the transformed plant cells against a biocide or antibiotic such as kanamycin, G 418, bleomycin, hygromycin or phosphinotricin etc. The individual marker employed should therefore allow the selection of transformed cells from cells, which lack the introduced

DNA.

For the introduction of DNA into a plant, besides transformation using *Agrobacteria*, there are many other techniques available. These techniques include the fusion of protoplasts, microinjection of DNA and electroporation, as well as ballistic methods and virus infection. From the transformed plant material, whole plants can be regenerated in a suitable medium, which contains antibiotics or biocides for the selection. The resulting plants can then be tested for the presence of introduced DNA. No special demands are placed on the plasmids in injection and electroporation. Simple plasmids, such as e.g. pUC-derivatives can be used. Should however whole plants be regenerated from such transformed cells the presence of a selectable marker gene is necessary. The transformed cells grow within the plants in the usual manner (see also McCormick et al.(1986) Plant Cell Reports 5: 81-84). These plants can be grown normally and crossed with plants, that possess the same transformed genes or different. The resulting hybrid individuals have the corresponding phenotypical properties.

Deposits

The following plasmids were deposited at the Deutschen Sammlung von Mikroorganismen (DSM) in Braunschweig, Germany on the 12.06.1992 (deposit number):

Plasmid p35S-anti-pot-SPS (DSM 7125)
Plasmid pB33-anti-pot-SPS (DSM 7124)

Description of the Figures

Fig. 1: Structure of the 35S-anti-pot-SPS gene

A = Fragment A: CaMV 35S promoter, nt 6909-7437 (Franck et al.,1980, Cell 21: 285-294)

B = Fragment B: sucrose phosphate synthase, EcoRV Fragment (nt 1 bis 2011), ca. 2000 bp, orientation: anti-sense

C = Fragment C: nt 11748-11939 of the T-DNA of the Ti-plasmid pTiACH5; Gielen et al., 1984, EMBO J 3: 835-846)

Fig. 2: Structure of the B33-anti-pot-SPS gene

A = Fragment A: B33 promoter of the patatin gene from *S. tuberosum,* (Rocha-Sosa et al., 1989, EMBO J 8: 23-29), ca 530 bp

B = Fragment B: sucrose phosphate synthase (s. Fig. 2), EcoRV fragment (nt 2011 bis 1), ca. 2000 bp, orientation: anti-sense

C = Fragment C: nt 11748-11939 of T-DNA of the Ti-plasmid pTiACH5 (Gielen et al., 1984, EMBO J 3: 835-846)

Fig. 3: shows the results of the transformation of transgenic potato plants.

Control = wild type plants
1-75 = individual transgenic plants

Fig. 4: shows the results of the transformation of potato plants

Control = wild type plants
3 - 20 = individual transgenic plants

In order to understand the examples forming the basis of this invention all the processes necessary for these tests and which are known per se will first of all be listed:

1. Cloning process

The vectors pUC 18/19 and M13mp10 series (Yanisch-Perron et al. (1985) Gene 33: 103-119), as well as the vector EMBL 3 (Frischauf et al. (1983) J Mol Biol 170: 827- 842) were used for cloning.

For the plant transformations, the gene constructs were cloned in the binary vector BIN 19 (Bevan (1984) Nucl. Acids Res 12: 8711-8720)

2. Bacterial strains

The *E. coli* strain BMH71-18 (Messing et al., Proc. Natl. Acad. Sci. USA (1977), 24, 6342-6346) or TB1 was used for the pUC and M13 mP vectors.

For the vector BIN19, the *E. coli* strain TB1 exclusively, was used. TB1 is a recombinant-negative, tetracycline-resistant derivative of strain JM101 (Yanisch-Perron et al., Gene (1985), 33, 103-119). The genotype of the TB1 strain is (Bart Barrel, personal communication): F'(traD36, proAB, lacI, lacZΔM15), Δ(lac, pro), SupE, thiS, recA, Sr1::Tn10(TcR).

The transformation of the plasmids into the potato plants was carried out using *Agrobacterium tumefaciens* strain LBA4404 (Bevan, (1984), Nucl. Acids Res. 12, 8711-8720).

3. Transformation of *Agrobacterium tumefaciens*

In the case of BIN19 derivatives, the insertion of the DNA

into the *Agrobacterium* was effected by direct transformation in accordance with the method of Holsters et al., (1978) (Mol Gene Genet 163: 181-187). The plasmid DNA of the transformed *Agrobacterium* was isolated in accordance with the method of Birnboim and Doly (1979) (Nucl Acids Res 7: 1513-1523) and was analysed by gel electrophoresis after suitable restriction cleavage.

4. Plant transformation

Ten small leaves, wounded with a scalpel, of a sterile potato culture were placed in 10 ml of MS medium with 2% sucrose containing 30-50 µl of an *Agrobacterium tumefaciens* overnight culture grown under selection. After 3-5 minutes gentle shaking, the leaves were laid out on MS medium of 1.6% glucose, 2 mg/l of zeatin ribose, 0.02 mg/l of naphthylacetic acid, 0.02 mg/l of gibberellic acid, 500 mg/l of claforan, 50 mg/l of kanamycin and 0.8% bacto agar. After incubation for one week at 25°C and 3000 lux, the claforan concentration in the medium was reduced by half.

5. SPS activity test

The SPS activity was determined according to the method of Siegel and Stitt (1990, Plant Science 66: 205-210) in a two stage analysis. To 180 µl of a solution of 50mM HEPES/KOH (pH 7.4), 5mM magnesium chloride, 5mM fructose-6-phosphate, 25mM glucose-6-phosphate and 6mM uridine-5'-diphosphoglucose 20 µl of probe was added and incubated for 10 minutes at 25°C. It was heated for 3 minutes at 95°C, to complete the reaction. After centrifuging, the supernatant was spectroscopically analysed for the liberation of uridine-5'-diphosphate, whereby a pyruvate-kinase coupling enzyme reaction was used. Preparations without hexose phosphate, as well as

the measurement of the recovery of added uridine-5'-diphosphate act as controls.

Examples

Example 1

Cloning of genes of the sucrose-phosphate-synthase from potato

Poly-A+ RNA was isolated from large leaves of spinach plants as well as potato plants grown in the greenhouse. Resulting from the poly-A+ RNA, a cDNA library in the expression vector Lambda Zap II was laid out. 100,000 Plaques of both libraries were separated from spinach using a rabbit antiserum directed against pure SPS protein in relation to immunologically cross reacting protein. (Sonnewald et al., 1992, in press). From the potato library, positively reacting clones were obtained. These clones were further purified by standard methods and, by *in vivo* excision, plasmids were obtained which carried a double stranded cDNA as an insertion. After testing the size of the insertions, individual clones were analysed by determining the primary sequence.

Example 2

Determination of the nucleotide sequence of the SPS from potato coding cDNA molecules and derivation of the corresponding amino acid sequences

The nucleotide sequences of the insertions obtained from Example 1, were determined by standard methods by means of the dideoxy method (Sanger et al. (1977) Proc. Natl. Acad. Sci. USA, 74, 5463-5467). The nucleotide sequences (Seq. ID No. 1 to Seq. ID No. 3) are described above. The amino acid sequences derived therefrom are also given.

Example 3

Construct of the plasmid p35s-anti-pot-SPS and insertion of gene 35s-anti-pot-sps in the genome of potato plants

The gene 35s-anti-pot-SPS consists of the three fragments A, B and C (see Fig 1).

The plasmid was prepared as follows:
From the pBluescript plasmid with the total insertion, an approximately 2 kb size fragment was prepared by EcoRV cleavage, and this was cloned in the SmaI cleavage site of the vector pBinAR (Höfgen & Willmitzer, 1990, Plant Sci., 66, 221-230). The vector pBinAR is a derivative of the binary vector BIN 19 (Bevan, 1984, Nucl. Acids Res. 12: 8711-8721) and was transferred using an *Agrobacterium tumefaciens* mediated transformation into potato. Intact, fertile plants were regenerated from the transformed cells.

As a result of the transformation, some transgenic potato plants were shown to have a reduced amount of RNA coding for the potato SPS (see Fig. 3). 50 µg total RNA in a Northern blot experiment was hybridised with the probe for SPS from potato.

Further the plants showed a reduction in SPS activity (see Table I).

Thus, by the transfer and expression of the gene 35s-anti-pot-SPS in potato plants, the amount of mRNA for the SPS protein which is formed, as well as the existing enzymatic activity can be significantly reduced.

Example 4

Construct of plasmid pB33-anti-pot-SPS and insertion of gene B33-anti-pot-SPS in the genome of potato plants

The gene B33-anti-pot-SPS consists of the three fragments A, B and C (see Fig 4). The plasmid was prepared in an analogous method to that described in Example 3, except a pBin 19 derivative was used as starting vector, that contains the B33 promoter of the patatin gene from *Solanum tuberosum* (Rocha-Sosa et al., 1989, EMBO J. 8: 23-29) in place of the 35S promoter of pBinAR.

The gene B33-anti-pot-SPS was transferred using an *Agrobacterium tumefaciens* mediated transformation into potato. Intact, fertile plants were regenerated from the transformed cells.

As a result of the transformation, some transgenic potato plants were shown with a reduced amount of RNA coding for the potato SPS (see Fig. 4). 50 µg total RNA in a Northern blot experiment was hybridised with the probe for SPS from potato.

Further the plants also showed a reduction of the SPS activity only in the tubers.

Thus, by the transfer and expression of the gene 35s-anti-pot-SPS in potato plants, the amount of mRNA for the SPS protein which is formed, as well as the existing enzymatic activity can be significantly reduced.

Table I

Results of the transformation of potato plants

1	2	3	4	5
Control	26.1	3.6	13.8	100
1-55	11.8	2.7	22.9	45
1-57	20.4	5.9	28.9	78
1-59	3.8	1.4	36.8	14.6
1-67	3.8	1.7	44.7	14.6
1-69	17.2	2.0	11.7	67
1-72	14.6	1.9	13.0	56
1-74	5.1	1.7	33.3	19.5

Column 1: Control = Wild type plants, numbers indicate individual transgenic plants

Column 2: Maximal speed of the enzyme reaction in the SPS activity test in nmol/min/mg.

Column 3: Speed in the SPS activity test in nmol/min/mg.

Column 4: Activity level of the SPS in %.

Column 5: Residual activity of the SPS in %.

CLAIMS

1. DNA sequence with the coding region for sucrose-phosphate-synthase (SPS) from *Solanum tuberosum* for the preparation of plants with modified sucrose concentration, characterised in that this sequence has the following nucleotide sequence (Seq. ID No.1):

CTATTCTCTC CCCTCCTTTT TCTCCTCTCT TCAACCCCAA AACTTCCCTT TCAAAGCCTT 60

TGCTTTCCCT TTCTCACTTA CCCAGATCAA CTAAGCCAAT TTGCTGTAGC CTCAGAAAAC 120

AGCATTCCCA GATTGAAAAA GAATCTTTTT CAGTACCCAA AAGTTGGGTT TCTCATGTCC 180

AGCAAGGATT AGCTGCTCTA GCTATTTCTT TAGCCCTTAA TTTTTGTCCA GTTGTGTCTT 240

CTGATTCTGC ATTGGCATCT GAATTTGATG TGTTAAATGA AGGGCCACCA AAGGACTCAT 300

ATGTAGTTGA TGATGCTGGT GTGCTTAGCA GGGTGACAAA GTCTGATTTG AAGGCATTGT 360

TGTCTGATGT GGAGAAGAGA AAAGGCTTCC ACATTAATTT CATCACTGTC CGCAAGCTCA 420

CTAGCAAAGC TGATGCTTTT GAGTATGCTG ACCAAGTTTT GGAGAAGTGG TACCCTAGTG 480

TTGAACAAGG AAATGATAAG GGTATAGTTG TGCTTGTTAC AAGTCAAAAG GAAGGCGCAA 540

TAACCGGTGG CCCTGATTTT GTAAAGGCCG TTGGAGATAC TGTTCTTGAT GCTACCGTCT 600

CAGAGAACCT TCCAGTGTTG GCTACTGAAG AGAAGTACAA TGAAGCAGTT TTCAGCACTG 660

CCACACGTCT TGTTGCAGCC ATTGATGGCC TTCCTGATCC TGGTGGACCC CAACTCAAGG 720

ATAACAAAAG AGAGTCCAAC TTCAAATCCA GAGAGGAAAC TGATGAGAAA AGAGGACAAT 780

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TCACACTTGT GGTTGGTGGG CTGTTAGTGA TTGCTTTTGT TGTTCCTATG GCTCAATACT  840

ATGCATATGT TTCAAAGAAG TGAACTGTCT GATTCTGGAA AGTTACATTT TCGTGAGATT  900

TGAGTAAGCA TGTATATTAT CGTGTACAAA ATGGTCCATT CGGAAATGAC TGATTC      956

ATG AGA TAT TTA AAA AGG ATA AAT ATG AAG ATT TGG ACC TCC CCT        1001
Met Arg Tyr Leu Lys Arg Ile Asn Met Lys Ile Trp Thr Ser Pro
1               5                   10                  15

AAC ATA ACG GAT ACT GCC ATT TCT TTT TCA GAG ATG CTG ACG CCA        1046
Asn Ile Thr Asp Thr Ala Ile Ser Phe Ser Glu Met Leu Thr Pro
                20                  25                  30

ATA AGT ACA GAC GGC TTG ATG ACT GAG ATG GGG GAG AGT AGT GGT        1091
Ile Ser Thr Asp Gly Leu Met Thr Glu Met Gly Glu Ser Ser Gly
                35                  40                  45

GCT TAT ATT ATT CGC ATT CCT TTT GGA CCA AGA GAG AAA TAT ATT        1136
Ala Tyr Ile Ile Arg Ile Pro Phe Gly Pro Arg Glu Lys Tyr Ile
                50                  55                  60

CCA AAA GAA CAG CTA TGG CCC TAT ATT CCC GAA TTT GTT GAT GGT        1181
Pro Lys Glu Gln Leu Trp Pro Tyr Ile Pro Glu Phe Val Asp Gly
                65                  70                  75

GCA CTT AAC CAT ATT ATT CAA ATG TCC AAA GTT CTT GGG GAG CAA        1226
Ala Leu Asn His Ile Ile Gln Met Ser Lys Val Leu Gly Glu Gln
                80                  85                  90

ATT GGT AGT GGC TAT CCT GTG TGG CCT GTT GCC ATA CAC GGA CAT        1271
Ile Gly Ser Gly Tyr Pro Val Trp Pro Val Ala Ile His Gly His
                95                  100                 105
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TAT GCT GAT GCT GGC GAC TCA GCT GCT CTC CTG TCA GGT GCT TTA      1316
Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
                110                 115                 120

AAT GTA CCA ATG CTT TTC ACT GGT CAC TCA CTT GGT AGA GAT AAG      1361
Asn Val Pro Met Leu Phe Thr Gly His Ser Leu Gly Arg Asp Lys
                125                 130                 135

TTG GAG CAA CTG TTG CGA CAA GGT CGT TTG TCA AAG GAT GAA ATA      1406
Leu Glu Gln Leu Leu Arg Gln Gly Arg Leu Ser Lys Asp Glu Ile
                140                 145                 150

AAC TCA ACC TAC AAG ATA ATG CGG AGA ATA GAG GCT GAA GAA TTA      1451
Asn Ser Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu
                155                 160                 165

ACT CTT GAT GCT TCC GAA ATT GTC ATC ACT AGT ACA AGA CAG GAG      1496
Thr Leu Asp Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu
                170                 175                 180

ATT GAC GAG CAA TGG CGT TTG TAT GAT GGG TTT GAT CCA ATA TTA      1541
Ile Asp Glu Gln Trp Arg Leu Tyr Asp Gly Phe Asp Pro Ile Leu
                185                 190                 195

GAG CGT AAG TTA CGT GCA AGG ATC AAG CGC AAT GTC AGC TGT TAT      1586
Glu Arg Lys Leu Arg Ala Arg Ile Lys Arg Asn Val Ser Cys Tyr
                200                 205                 210

GGC AGG TTT ATG CCT CGT ATG GCT GTA ATT CCT CCT GGG ATG GAG      1631
Gly Arg Phe Met Pro Arg Met Ala Val Ile Pro Pro Gly Met Glu
                215                 220                 225
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TTC CAC CAT ATT GTG CCA CAT GAA GGT GAC ATG GAT GGA GAA ACA      1676
Phe His His Ile Val Pro His Glu Gly Asp Met Asp Gly Glu Thr
                230                 235                 240

GAA GGA AGT GAA GAT GGG AAG ACC CCG GAT CCA CCT ATT TGG GCA      1721
Glu Gly Ser Glu Asp Gly Lys Thr Pro Asp Pro Pro Ile Trp Ala
                245                 250                 255

GAG ATT ATG CGC TTC TTT TCT AAT CCA AGG AAG CCT ATG ATA CTC      1766
Glu Ile Met Arg Phe Phe Ser Asn Pro Arg Lys Pro Met Ile Leu
                260                 265                 270

GCA CTT GCT AGG CCT GAT CCC AAG AAG AAC CTC ACT ACT TTA GTG      1811
Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn Leu Thr Thr Leu Val
                275                 280                 285

AAA GCA TTT GGT GAA TGT CGT CCA TTG AGA GAG CTT GCT AAT CTT      1856
Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn Leu
                290                 295                 300

ACT TTG ATA ATG GGT AAT CGA GAT AAT ATC GAC GAA ATG TCT AGC      1901
Thr Leu Ile Met Gly Asn Arg Asp Asn Ile Asp Glu Met Ser Ser
                305                 310                 315

ACC AAT TCT GCA CTT CTT CTT TCA ATC TTG AAA ATG ATA GAT AAG      1946
Thr Asn Ser Ala Leu Leu Leu Ser Ile Leu Lys Met Ile Asp Lys
                320                 325                 330

TAT GAT CTT TAT GGT CAA GTA GCT TAT CCT AAA CAC CAC AAG CAG      1991
Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys Gln
                335                 340                 345

TCA GAT GTT CCT GAT ATC TAC CGT CTT GCT GCA AAG ACT AAG GGT      2036
Ser Asp Val Pro Asp Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly
                350                 355                 360
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GTT TTT ATT AAT CCA GCT TTT ATT GAG CCT TTT GGA CTG ACT TTG 2081
Val Phe Ile Asn Pro Ala Phe Ile Glu Pro Phe Gly Leu Thr Leu
365 370 375

ATT GAG GCA GCA GCT TAT GGT CTC CCA ATG GTA GCC ACA AAA AAT 2126
Ile Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Lys Asn
380 385 390

GGA GGA CCT GTT GAT ATA CAT AGG GTT CTT GAC AAT GGT CTC TTA 2171
Gly Gly Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Leu Leu
395 400 405

GTG GAT CCC CAT GAT CAG CAG GCA ATT GCT GAT GCT CTT TTG AAG 2216
Val Asp Pro His Asp Gln Gln Ala Ile Ala Asp Ala Leu Leu Lys
410 415 420

TTG GTT GCT GAT AAG CAA CTG TGG GCT AAA TGC AGG GCA AAT GGA 2261
Leu Val Ala Asp Lys Gln Leu Trp Ala Lys Cys Arg Ala Asn Gly
425 430 435

TTA AAA AAT ATC CAC CTT TTC TCA TGG CCC GAG CAC TGT AAA ACT 2306
Leu Lys Asn Ile His Leu Phe Ser Trp Pro Glu His Cys Lys Thr
440 445 450

TAT CTA TCC CGG ATA GCT AGC TGC AAA CCA AGG CAA CCA CGC TGG 2351
Tyr Leu Ser Arg Ile Ala Ser Cys Lys Pro Arg Gln Pro Arg Trp
455 460 465

CTG AGA TCC ATT GAT GAT GAT GAT GAA AAT TCA GAA ACA GAT TCA 2396
Leu Arg Ser Ile Asp Asp Asp Asp Glu Asn Ser Glu Thr Asp Ser
470 475 480

CCT AGT GAT TCC TTG AGA GAT ATT CAT GAT ATA TCT CTG AAT TTG 2441
Pro Ser Asp Ser Leu Arg Asp Ile His Asp Ile Ser Leu Asn Leu
485 490 495

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AGA TTT TCA TTA GAT GGG GAA AAG AAT GAC AAT AAA GAA AAT GCT      2486
Arg Phe Ser Leu Asp Gly Glu Lys Asn Asp Asn Lys Glu Asn Ala
                500                 505                 510

GAT AAT ACA TTA GAC CCC GAA GTT CGA AGG AGC AAG TTA GAG AAT      2531
Asp Asn Thr Leu Asp Pro Glu Val Arg Arg Ser Lys Leu Glu Asn
                515                 520                 525

GCT GTT TTG TCC TTA TCT AAG GGT GCA CTG AAG AGC ACA TCA AAA      2576
Ala Val Leu Ser Leu Ser Lys Gly Ala Leu Lys Ser Thr Ser Lys
                530                 535                 540

TCT TGG TCG TCA GAC AAG GCA GAC CAA AAC CCT GGT GCT GGT AAA      2621
Ser Trp Ser Ser Asp Lys Ala Asp Gln Asn Pro Gly Ala Gly Lys
                545                 550                 555

TTC CCA GCG ATT AGG AGG AGG CGA CAT ATT TTT GTT ATT GCA GTG      2666
Phe Pro Ala Ile Arg Arg Arg Arg His Ile Phe Val Ile Ala Val
                560                 560                 565

GAT TGT GAT GCT AGC TCA GGA CTC TCT GGA AGT GTG AAA AAG ATA      2711
Asp Cys Asp Ala Ser Ser Gly Leu Ser Gly Ser Val Lys Lys Ile
                570                 575                 580

TTT GAG GCT GTA GAG AAG GAA AGG GCA GAG GGT TCC ATT GGA TTT      2756
Phe Glu Ala Val Glu Lys Glu Arg Ala Glu Gly Ser Ile Gly Phe
                585                 590                 595

ATC CTG GCT ACA TCT TTC AAT ATA TCA GAA GTA CAG TCT TTC CTG      2801
Ile Leu Ala Thr Ser Phe Asn Ile Ser Glu Val Gln Ser Phe Leu
                600                 605                 610

CTT TCA GAG GGC ATG AAT CCT ACT GAT TTT GAT GCT TAC ATA TGC      2846
Leu Ser Glu Gly Met Asn Pro Thr Asp Phe Asp Ala Tyr Ile Cys
                615                 620                 625
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AAT AGT GGT GGT GAT CTT TAT TAT TCG TCC TTC CAT TCT GAG CAA        2891
Asn Ser Gly Gly Asp Leu Tyr Tyr Ser Ser Phe His Ser Glu Gln
                630                 635                 640

AAT CCT TTT GTA GTT GAC TTG TAC TAT CAC TCA CAT ATT GAG TAT        2936
Asn Pro Phe Val Val Asp Leu Tyr Tyr His Ser His Ile Glu Tyr
                645                 650                 655

CGT TGG GGG GGC GAA GGA TTG AGA AAG ACT TTG GTG CGT TGG GCC        2981
Arg Trp Gly Gly Glu Gly Leu Arg Lys Thr Leu Val Arg Trp Ala
                660                 665                 670

GCC TCT ATC ATT GAT AAG AAT GGT GAA AAT GGA GAT CAC ATT GTT        3026
Ala Ser Ile Ile Asp Lys Asn Gly Glu Asn Gly Asp His Ile Val
                675                 680                 685

GTT GAG GAT GAA GAC AAT TCA GCT GAC TAC TGC TAT ACT TTC AAA        3071
Val Glu Asp Glu Asp Asn Ser Ala Asp Tyr Cys Tyr Thr Phe Lys
                690                 695                 700

GTC TGC AAG CCT GGG ACG GTT CCT CCA TCT AAA GAG CTT AGA AAA        3116
Val Cys Lys Pro Gly Thr Val Pro Pro Ser Lys Glu Leu Arg Lys
                705                 710                 715

GTA ATG CGA ATT CAG GCA CTT CGT TGT CAC GCT GTT TAT TGT CAA        3161
Val Met Arg Ile Gln Ala Leu Arg Cys His Ala Val Tyr Cys Gln
                720                 725                 730

AAT GGG AGT AGG ATT AAT GTG ATC CCT GTA CTG GCA TCT CGG TCC        3206
Asn Gly Ser Arg Ile Asn Val Ile Pro Val Leu Ala Ser Arg Ser
                735                 740                 745

CAA GCA CTC AGG TAC TTA TAT CTG CGA TGG GGA ATG GAC TTG TCG        3251
Gln Ala Leu Arg Tyr Leu Tyr Leu Arg Trp Gly Met Asp Leu Ser
                750                 755                 760
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AAG TTG GTG GTT TTC GTC GGA GAA AGT GGT GAT ACC GAT TAT GAA       3296
Lys Leu Val Val Phe Val Gly Glu Ser Gly Asp Thr Asp Tyr Glu
                765                 770                 775

GGA TTA ATC GGT GGT CTA CGC AAG GCT GTC ATA ATG AAA GGC CTC       3341
Gly Leu Ile Gly Gly Leu Arg Lys Ala Val Ile Met Lys Gly Leu
                780                 785                 790

TGC ACT AAT GCA AGC AGC TTA ATT CAC GGT AAT AGG AAT TAC CCG       3386
Cys Thr Asn Ala Ser Ser Leu Ile His Gly Asn Arg Asn Tyr Pro
                795                 800                 805

CTA TCT GAT GTT TTA CCA TTC GAC AGC CCT AAT GTC ATC CAA GCG       3431
Leu Ser Asp Val Leu Pro Phe Asp Ser Pro Asn Val Ile Gln Ala
                810                 815                 820

GAC GAG GAA TGT AGC AGC ACC GAA ATC CGT TGC TTA CTG GTG AAA       3476
Asp Glu Glu Cys Ser Ser Thr Glu Ile Arg Cys Leu Leu Val Lys
                825                 830                 835

CTA GCG GTA CTC AAA GGA TAATACCCTT CCCCCTTTGA TTGTCAAAAA          3524
Leu Ala Val Leu Lys Gly
                840

CCTATATGAG CTATAAGACT ATGCCATGAA AAGAATGGCC ATCCATTTGG CTTGTCTTTT 3584

GAAGCTGTTA ATACTTTTCA ACAGACTACA AAATGAGATG AGTCCTTTGA TCCTCTTTAA 3644

AGGACATAAA AGCTTTATGC AAGAACCAGT GCTGTAAAGT TATAGAATTT CTTTTGCTAT 3704

ATATGACATT CGACAGAACC TGTTCCGGTT CATCGA   3740
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2. DNA sequence with the coding region for sucrose-phosphate-synthase (SPS) from *Solanum tuberosum* for the preparation of plants with modified sucrose concentration, characterised in that this sequence has the following nucleotide sequence (Seq. ID No.2):

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ATTTTTTTCT CTAAGTTCTC TCTCGCTGTC CTTATCATTT CACCACCTCC ATAAATCTAG  60

AAACATCTTT TCTACTCCGT TAATCTCTCT AGCACACGGC GGAGGAGTGC GGCGGAGGAG 120

ATG GCG GGA AAC GAT TGG ATT AAC AGT TAC TTA GAG GCG ATA CTG        165
Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu
1               5                  10                  15

GAT GTT GGA CCA GGG CTA GAT GAT AAG AAG TCA TCG TTG TTG TTG        210
Asp Val Gly Pro Gly Leu Asp Asp Lys Lys Ser Ser Leu Leu Leu
                20                  25                  30

AGA GAA AGA GGG AGG TTT AGT CCG ACG AGG TAC TTT GTT GAG GAA        255
Arg Glu Arg Gly Arg Phe Ser Pro Thr Arg Tyr Phe Val Glu Glu
                35                  40                  45

GTT ATT ACT GGA TTC GAT GAG ACT GAT TTG CAT CGT TCG TGG ATC        300
Val Ile Thr Gly Phe Asp Glu Thr Asp Leu His Arg Ser Trp Ile
                50                  55                  60

CGA GCA CAA GCT ACT CGG AGT CCG CAG AGA AGG AAT ACT AGG CTC        345
Arg Ala Gln Ala Thr Arg Ser Pro Gln Arg Arg Asn Thr Arg Leu
                65                  70                  75

GAG AAT ATG TGC TGG AGG ATT TGG AAT TTG GCT CGC CAG AAA AAG        390
Glu Asn Met Cys Trp Arg Ile Trp Asn Leu Ala Arg Gln Lys Lys
                80                  85                  90
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CAG CTT GAG GGA GAG CAA GCT CAG TGG ATG GCA AAA CGC CGT CAA        435
Gln Leu Glu Gly Glu Gln Ala Gln Trp Met Ala Lys Arg Arg Gln
                95                  100                 105

GAA CGT GAA AGA GGT CGC AGA GAA GCA GTT GCT GAT ATG TCA GAG        480
Glu Arg Glu Arg Gly Arg Arg Glu Ala Val Ala Asp Met Ser Glu
                110                 115                 120

GAT CTA TCT GAG GGA GAG AAA GGA GAT ATA GTC GCT GAC ATG TCA        525
Asp Leu Ser Glu Gly Glu Lys Gly Asp Ile Val Ala Asp Met Ser
                125                 130                 135

TCT CAT GGT GAA AGT ACC AGA GGC CGA TTG CCT AGA ATC AGT TCT        570
Ser His Gly Glu Ser Thr Arg Gly Arg Leu Pro Arg Ile Ser Ser
                140                 145                 150

GTT GAG ACA ATG GAA GCA TGG GTC AGT CAG CAG AGA GGA AAG AAG        615
Val Glu Thr Met Glu Ala Trp Val Ser Gln Gln Arg Gly Lys Lys
                155                 160                 165

CTT TAT ATC GTG CTT ATA AGT TTA CAT GGT TTA ATT CGG GGT GAG        660
Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Ile Arg Gly Glu
                170                 175                 180

AAT ATG GAG CTT GGA CGG GAT TCT GAT ACT GGT GGT CAG GTG AAG        705
Asn Met Glu Leu Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys
                185                 190                 195

TAT GTT GTT GAA CTT GCG AGG GCC TTA GGG TCG ATG CCA GGT GTA        750
Tyr Val Val Glu Leu Ala Arg Ala Leu Gly Ser Met Pro Gly Val
                200                 205                 210

TAT CGG GTT GAC TTG CTT ACT AGA CAA GTA TCT TCA CCA GAA GTA        795
Tyr Arg Val Asp Leu Leu Thr Arg Gln Val Ser Ser Pro Glu Val
                215                 220                 225
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GAT TGG AGC TAT GGT GAG CCG ACA GAG ATG CTG ACG CCA ATA AGT        840
Asp Trp Ser Tyr Gly Glu Pro Thr Glu Met Leu Thr Pro Ile Ser
                230                 235                 240

ACA GAC GGC TTG ATG ACT GAG ATG GGG GAG AGT AGT GGT GCT TAT        885
Thr Asp Gly Leu Met Thr Glu Met Gly Glu Ser Ser Gly Ala Tyr
                245                 250                 255

ATT ATT CGC ATT CCT TTT GGA CCA AGA GAG AAA TAT ATT CCA AAA        930
Ile Ile Arg Ile Pro Phe Gly Pro Arg Glu Lys Tyr Ile Pro Lys
                260                 265                 270

GAA CAG CTA TGG CCC TAT ATT CCC GAA TTT GTT GAT GGT GCA CTT        975
Glu Gln Leu Trp Pro Tyr Ile Pro Glu Phe Val Asp Gly Ala Leu
                275                 280                 285

AAC CAT ATT ATT CAA ATG TCC AAA GTT CTT GGG GAG CAA ATT GGT       1020
Asn His Ile Ile Gln Met Ser Lys Val Leu Gly Glu Gln Ile Gly
                290                 295                 300

AGT GGC TAT CCT GTG TGG CCT GTT GCC ATA CAC GGA CAT TAT GCT       1065
Ser Gly Tyr Pro Val Trp Pro Val Ala Ile His Gly His Tyr Ala
                305                 310                 315

GAT GCT GGC GAC TCA GCT GCT CTC CTG TCA GGT GCT TTA AAT GTA       1110
Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu Asn Val
                320                 330                 335

CCA ATG CTT TTC ACT GGT CAC TCA CTT GGT AGA GAT AAG TTG GAG       1155
Pro Met Leu Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu Glu
                340                 345                 350

CAA CTG TTG GCA CAA GGT CGA AAG TCA AAG GAT GAA ATA AAC TCA       1200
Gln Leu Leu Ala Gln Gly Arg Lys Ser Lys Asp Glu Ile Asn Ser
                355                 360                 365
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ACC TAC AAG ATA ATG CGG AGA ATA GAG GCT GAA GAA TTA ACT CTT      1245
Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Thr Leu
                370                 375                 380

GAT GCT TCC GAA ATT GTC ATC ACT AGT ACA AGA CAG GAG ATT GAC      1290
Asp Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Asp
                385                 390                 395

GAG CAA TGG CGT TTG TAT GAT GGG TTT GAT CCA ATA TTA GAG CGT      1335
Glu Gln Trp Arg Leu Tyr Asp Gly Phe Asp Pro Ile Leu Glu Arg
                400                 405                 410

AAG TTA CGT GCA AGG ATC AAG CGC AAT GTC AGC TGT TAT GGC AGG      1380
Lys Leu Arg Ala Arg Ile Lys Arg Asn Val Ser Cys Tyr Gly Arg
                415                 420                 425

TTT ATG CCT CGT ATG GCT GTA ATT CCT CCT GGG ATG GAG TTC CAC      1425
Phe Met Pro Arg Met Ala Val Ile Pro Pro Gly Met Glu Phe His
                430                 435                 440

CAT ATT GTG CCA CAT GAA GGT GAC ATG GAT GGT GAA ACA GAA GGA      1470
His Ile Val Pro His Glu Gly Asp Met Asp Gly Glu Thr Glu Gly
                445                 450                 455

AGT GAA GAT GGG AAG ACC CCG GAT CCA CCT ATT TGG GCA GAG ATT      1515
Ser Glu Asp Gly Lys Thr Pro Asp Pro Pro Ile Trp Ala Glu Ile
                460                 465                 470

ATG CGC TTC TTT TCT AAT CCA AGG AAG CCT ATG ATA CTC GCA CTT      1560
Met Arg Phe Phe Ser Asn Pro Arg Lys Pro Met Ile Leu Ala Leu
                475                 480                 485

GCT AGG CCT GAT CCC AAG AAG AAC CTC ACT ACT TTA GTG AAA GCA      1605
Ala Arg Pro Asp Pro Lys Lys Asn Leu Thr Thr Leu Val Lys Ala
                490                 495                 500
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TTT GGT GAA TGT CGT CCA TTG AGA GAG CTT GCT AAT CTT ACT TTG      1650
Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn Leu Thr Leu
                505                 510                 515

ATA ATG GGT AAT CGA GAT AAT ATC GAC GAA ATG TCT AGC ACC AAT      1695
Ile Met Gly Asn Arg Asp Asn Ile Asp Glu Met Ser Ser Thr Asn
                520                 525                 530

TCT GCA CTT CTT CTT TCA ATC TTG AAA ATG ATA GAT AAG TAT GAT      1740
Ser Ala Leu Leu Leu Ser Ile Leu Lys Met Ile Asp Lys Tyr Asp
                535                 540                 540

CTT TAT GGT CAA GTA GCT TAT CCT AAA CAC CAC AAG CAG TCA GAT      1785
Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys Gln Ser Asp
                545                 550                 555

GTT CCT GAT ATC TAC CGT CTT GCT GCA AAG ACT AAG GGT GTT TTT      1830
Val Pro Asp Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly Val Phe
                560                 565                 570

ATT AAT CCA GCT TTT ATT GAG CCT TTT GGA CTG ACT TTG ATT GAG      1875
Ile Asn Pro Ala Phe Ile Glu Pro Phe Gly Leu Thr Leu Ile Glu
                575                 580                 585

GCA GCA GCT TAT GGT CTC CCA ATG GTA GCC ACA AAA AAT GGA GGA      1920
Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Lys Asn Gly Gly
                590                 595                 600

CCT GTT GAT ATA CAT AGG GTT CTT GAC AAT GGT CTC TTA GTG GAT      1965
Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Leu Leu Val Asp
                605                 610                 615

CCC CAT GAT CAG CAG GCA ATT GCT GAT GCT CTT TTG AAG TTG GTT      2010
Pro His Asp Gln Gln Ala Ile Ala Asp Ala Leu Leu Lys Leu Val
                620                 625                 630
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GCT GAT AAG CAA CTG TGG GCT AAA TGC AGG GCA AAT GGA TTA AAA      2055
Ala Asp Lys Gln Leu Trp Ala Lys Cys Arg Ala Asn Gly Leu Lys
                635                 640                 645

AAT ATC CAC CTT TTC TCA TGG CCC GAG CAC TGT AAA ACT TAT CTA      2100
Asn Ile His Leu Phe Ser Trp Pro Glu His Cys Lys Thr Tyr Leu
            650                 655                 660

TCC CGG ATA GCT AGC TGC AAA CCA AGG CAA CCA CGC TGG CTG AGA      2145
Ser Arg Ile Ala Ser Cys Lys Pro Arg Gln Pro Arg Trp Leu Arg
                665                 670                 675

TCC ATT GAT GAT GAT GAT GAA AAT TCA GAA ACA GAT TCA CCT AGT      2190
Ser Ile Asp Asp Asp Asp Glu Asn Ser Glu Thr Asp Ser Pro Ser
                680                 685                 690

GAT TCC TTG AGA GAT ATT CAT GAT ATA TCT CTG AAT TTG AGA TTT      2235
Asp Ser Leu Arg Asp Ile His Asp Ile Ser Leu Asn Leu Arg Phe
                695                 700                 705

TCA TTA GAT GGG GAA AAG AAT GAC AAT AAA GAA AAT GCT GAT AAT      2280
Ser Leu Asp Gly Glu Lys Asn Asp Asn Lys Glu Asn Ala Asp Asn
                710                 715                 720

ACA TTA GAC CCC GAA GTT CGA AGG AGC AAG TTA GAG AAT GCT GTT      2325
Thr Leu Asp Pro Glu Val Arg Arg Ser Lys Leu Glu Asn Ala Val
                725                 730                 735

TTG TCC TTA TCT AAG GGT GCA CTG AAG AGC ACA TCA AAA TCT TGG      2370
Leu Ser Leu Ser Lys Gly Ala Leu Lys Ser Thr Ser Lys Ser Trp
                740                 745                 750

TCG TCA GAC AAG GCA GAC CAA AAC CCT GGT GCT GGT AAA TTC CCA      2415
Ser Ser Asp Lys Ala Asp Gln Asn Pro Gly Ala Gly Lys Phe Pro
                755                 760                 765
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GCG ATT AGG AGG AGG CGA CAT ATT TTT GTT ATT GCA GTG GAT TGT 2460
Ala Ile Arg Arg Arg Arg His Ile Phe Val Ile Ala Val Asp Cys
770 775 780

GAT GCT AGC TCA GGA CTC TCT GGA AGT GTG AAA AAG ATA TTT GAG 2505
Asp Ala Ser Ser Gly Leu Ser Gly Ser Val Lys Lys Ile Phe Glu
785 790 795

GCT GTA GAG AAG GAA AGG GCA GAG GGT TCC ATT GGA TTT ATC CTG 2550
Ala Val Glu Lys Glu Arg Ala Glu Gly Ser Ile Gly Phe Ile Leu
800 805 810

GCT ACA TCT TTC AAT ATA TCA GAA GTA CAG TCT TTC CTG CTT TCA 2595
Ala Thr Ser Phe Asn Ile Ser Glu Val Gln Ser Phe Leu Leu Ser
815 820 825

GAG GGC ATG AAT CCT ACT GAT TTT GAT GCT TAC ATA TGC AAT AGT 2640
Glu Gly Met Asn Pro Thr Asp Phe Asp Ala Tyr Ile Cys Asn Ser
830 835 840

GGT GGT GAT CTT TAT TAT TCG TCC TTC CAT TCT GAG CAA AAT CCT 2685
Gly Gly Asp Leu Tyr Tyr Ser Ser Phe His Ser Glu Gln Asn Pro
845 850 855

TTT GTA GTT GAC TTG TAC TAT CAC TCA CAT ATT GAG TAT CGT TGG 2730
Phe Val Val Asp Leu Tyr Tyr His Ser His Ile Glu Tyr Arg Trp
860 865 870

GGG GGC GAA GGA TTG AGA AAG ACT TTG GTG CGT TGG GCC GCC TCT 2775
Gly Gly Glu Gly Leu Arg Lys Thr Leu Val Arg Trp Ala Ala Ser
875 880 885

ATC ATT GAT AAG AAT GGT GAA AAT GGA GAT CAC ATT GTT GTT GAG 2820
Ile Ile Asp Lys Asn Gly Glu Asn Gly Asp His Ile Val Val Glu
890 895 900

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GAT GAA GAC AAT TCA GCT GAC TAC TGC TAT ACT TTC AAA GTC TGC      2865
Asp Glu Asp Asn Ser Ala Asp Tyr Cys Tyr Thr Phe Lys Val Cys
                905                 910                 915

AAG CCT GGG ACG GTT CCT CCA TCT AAA GAG CTT AGA AAA GTA ATG      2910
Lys Pro Gly Thr Val Pro Pro Ser Lys Glu Leu Arg Lys Val Met
            920                 925                 930

CGA ATT CAG GCA CTT CGT TGT CAC GCT GTT TAT TGT CAA AAT GGG      2955
Arg Ile Gln Ala Leu Arg Cys His Ala Val Tyr Cys Gln Asn Gly
                935                 940                 945

AGT AGG ATT AAT GTG ATC CCT GTA CTG GCA TCT CGG TCC CAA GCA      3000
Ser Arg Ile Asn Val Ile Pro Val Leu Ala Ser Arg Ser Gln Ala
                950                 955                 960

CTC AGG TAC TTA TAT CTG CGA TGG GGA ATG GAC TTG TCG AAG TTG      3045
Leu Arg Tyr Leu Tyr Leu Arg Trp Gly Met Asp Leu Ser Lys Leu
                965                 970                 975

GTG GTT TTC GTC GGA GAA AGT GGT GAT ACC GAT TAT GAA GGA TTA      3090
Val Val Phe Val Gly Glu Ser Gly Asp Thr Asp Tyr Glu Gly Leu
                980                 985                 990

ATC GGT GGT CTA CGC AAG GCT GTC ATA ATG AAA GGC CTC TGC ACT      3135
Ile Gly Gly Leu Arg Lys Ala Val Ile Met Lys Gly Leu Cys Thr
                995                 1000                1005

AAT GCA AGC AGC TTA ATT CAC GGT AAT AGG AAT TAC CCG CTA TCT      3180
Asn Ala Ser Ser Leu Ile His Gly Asn Arg Asn Tyr Pro Leu Ser
                1010                1015                1020

GAT GTT TTA CCA TTC GAC AGC CCT AAT GTC ATC CAA GCG GAC GAG      3225
Asp Val Leu Pro Phe Asp Ser Pro Asn Val Ile Gln Ala Asp Glu
                1025                1030                1035
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GAA TGT AGC AGC ACC GAA ATC CGT TGC TTA CTG GAG AAA CTA GCG 3270
Glu Cys Ser Ser Thr Glu Ile Arg Cys Leu Leu Glu Lys Leu Ala
1040 1045 1050

GTA CTC AAA GGA TAA TACCCTTCCC CCTTTGATTG TCAAAAACCT 3315
Val Leu Lys Gly End
1054

ATATGAGCTA TAAGACTATG CCATGAAAAG AATGGCCATC CATTTGGCTT GTCTTTTGAA 3375

GCTGTTAATA CTTTTCAACA GACTACAAAA TGAGATGAGT CCTTTGATCC TCTTTAAAGG 3435

ACATAAAAGC TTTATGCAAG AACCAGTGCT GTAAAGTTAT AGAATTTCTT TTGCTATATA 3495

TGACATTCGA CAGAACCAGT TCCGGTTCAT CGAGAAAAAG AAATAAATTT CAACTTATAA 3555

ACATGCCTGA TCATGTAAAT TATCATATAC ATCCATCGGA AGGCATTATC GATGGGTTAT 3615

CAGATTTTTT 3625

3. DNA sequence with the coding region for sucrose-phosphate-synthase (SPS) from *Solanum tuberosum* for the preparation of plants with modified sucrose concentration, characterised in that this sequence has the following nucleotide sequence (Seq. ID No.3):

ATTTTTT TCTCTAAATT CTCTCTCACT GTCCTTATCA TTTCACCACC TCCATAAATC 57

TAGAAACATC TTTTCTATTC CGTTAATCTC TCTAGCACAC GGCGGAGTGC GGCGGAGGAG 117

ATG GCG GGA AAC GAC TGG ATT AAC AGT TAC TTA GAG GCG ATA CTG 162
Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu
1 5 10 15

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GAT GTA GGA CCA GGG CTA GAT GAT AAG AAA TCA TCG TTG TTG TTG      207
Asp Val Gly Pro Gly Leu Asp Asp Lys Lys Ser Ser Leu Leu Leu
                20                  25                  30

AGA GAA AGA GGG AGG TTT AGT CCG ACG AGG TAC TTT GTT GAG GAA      252
Arg Glu Arg Gly Arg Phe Ser Pro Thr Arg Tyr Phe Val Glu Glu
                35                  40                  45

GTT ATT ACT GGA TTC GAT GAG ACT GAT TTG CAT CGC TCG TGG ATC      297
Val Ile Thr Gly Phe Asp Glu Thr Asp Leu His Arg Ser Trp Ile
                50                  55                  60

CGA GCA CAA GCT ACT CGG AGT CCG CAG GAG AGG AAT ACT AGG CTC      342
Arg Ala Gln Ala Thr Arg Ser Pro Gln Glu Arg Asn Thr Arg Leu
                65                  70                  75

GAG AAT ATG TGC TGG AGG ATT TGG AAT TTG GCT CGC CAG AAA AAG      387
Glu Asn Met Cys Trp Arg Ile Trp Asn Leu Ala Arg Gln Lys Lys
                80                  85                  90

CAG CTT GAG GGA GAG CAA GCT CAG TGG ATG GCA AAA CGC CGT CAA      432
Gln Leu Glu Gly Glu Gln Ala Gln Trp Met Ala Lys Arg Arg Gln
                95                  100                 105

GAA CGT GAG AGA GGT CGC AGA GAA GCA GTT GCT GAT ATG TCA GAG      477
Glu Arg Glu Arg Gly Arg Arg Glu Ala Val Ala Asp Met Ser Glu
                110                 115                 120

GAT CTA TCT GAG GGA GAG AAA GGA GAT ATA GTC GCT GAC ATG TCA      522
Asp Leu Ser Glu Gly Glu Lys Gly Asp Ile Val Ala Asp Met Ser
                125                 130                 135

TCT CAT GGT GAA AGT ACC AGA GGC CGA TTG CCT AGA ATC AGT TCT      567
Ser His Gly Glu Ser Thr Arg Gly Arg Leu Pro Arg Ile Ser Ser
                140                 145                 150
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GTT GAG ACA ATG GAA GCA TGG GTC AGT CAG CAG AGA GGA AAG AAG        612
Val Glu Thr Met Glu Ala Trp Val Ser Gln Gln Arg Gly Lys Lys
                155                 160                 165

CTT TAT ATC GTG CTT ATA AGT TTA CAT GGT TTA ATT CGG GGT GAG        657
Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Ile Arg Gly Glu
                170                 175                 180

AAT ATG GAG CTT GGA CGG GAT TCT GAT ACT GGT GGT CAG GTG AAG        702
Asn Met Glu Leu Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys
                185                 190                 195

TAT GTA GTT GGA GCA ACT GTT GCA CAA GGT CGT TTG TCA AAG GAT        747
Tyr Val Val Gly Ala Thr Val Ala Gln Gly Arg Leu Ser Lys Asp
                200                 205                 210

GAA ATA AAC TCA ACC TAC AAG ATA ATG CGG AGA ATA GAG GCT GAA        792
Glu Ile Asn Ser Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu
                215                 220                 225

GAA TTA ACT CTT GAT GCT TCC GAA ATT GTC ATC ACT AGT ACA AGA        837
Glu Leu Thr Leu Asp Ala Ser Glu Ile Val Ile Thr Ser Thr Arg
                230                 235                 240

CAG GAG ATT GAC GAG CAA TGG CGT TTG TAT GAT GGG TTT GAT CCA        882
Gln Glu Ile Asp Glu Gln Trp Arg Leu Tyr Asp Gly Phe Asp Pro
                245                 250                 255

ATA TTA GAG CGT AAG TTA CGT GCA AGG ATC AAG CGC AAT GTC AGC        927
Ile Leu Glu Arg Lys Leu Arg Ala Arg Ile Lys Arg Asn Val Ser
                260                 265                 270

TGT TAT GGC AGG TTT ATG CCT CGT ATG GCT GTA ATT CCT CCT GGG        972
Cys Tyr Gly Arg Phe Met Pro Arg Met Ala Val Ile Pro Pro Gly
                275                 280                 285
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ATG GAG TTC CAC CAT ATT GTG CCA CAT GAA GGT GAC ATG GAT GGT 1017
Met Glu Phe His His Ile Val Pro His Glu Gly Asp Met Asp Gly
290 295 300

GAA ACA GAA GGA AGT GAA GAT GGA AAG ACC CCG GAT CCA CCT ATT 1062
Glu Thr Glu Gly Ser Glu Asp Gly Lys Thr Pro Asp Pro Pro Ile
305 310 315

TGG GCA GAG ATT ATG CGC TTC TTT TCT AAT CCA AGG AAG CCT ATG 1107
Trp Ala Glu Ile Met Arg Phe Phe Ser Asn Pro Arg Lys Pro Met
320 330 335

ATA CTC GCA CTT GCT AGG CCT GAT CCC AAG AAG AAC CTC ACT ACT 1152
Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn Leu Thr Thr
340 345 350

TTA GTG AAA GCA TTT GGT GAA TGT CGT CCA TTG AGA GAC CTT GCT 1197
Leu Val Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Asp Leu Ala
355 360 365

AAT CTT ACT TTG ATA ATG GGT AAT CGA GAT AAT ATC GAC GAA ATG 1242
Asn Leu Thr Leu Ile Met Gly Asn Arg Asp Asn Ile Asp Glu Met
370 375 380

TCT AGC ACC AAT TCT GCA CTT CTT CTT TCA ATC TTG AAG ATG ATA 1287
Ser Ser Thr Asn Ser Ala Leu Leu Leu Ser Ile Leu Lys Met Ile
385 390 395

GAT AAG TAT GAT CTT TAT GGT CTA GTA GCT TAT CCT AAA CAC CAC 1332
Asp Lys Tyr Asp Leu Tyr Gly Leu Val Ala Tyr Pro Lys His His
400 405 410

AAG CAG TCA GAT GTT CCT GAT ATC TAC CGT CTT GCT GCA AAG ACT 1377
Lys Gln Ser Asp Val Pro Asp Ile Tyr Arg Leu Ala Ala Lys Thr
415 420 425

AAG GGT GTT TTT ATT AAT CCA GCT TTT ATT GAG CCT TTT GGA CTG 1422
Lys Gly Val Phe Ile Asn Pro Ala Phe Ile Glu Pro Phe Gly Leu
430 435 440

ACT TTG ATT GAG GCA GCA GCT TAT GGT CTC CCA ATG GTA GCC ACA 1467
Thr Leu Ile Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr
445 450 455

AAA AAT GGA GGA CCT GTT GAT ATA CAT AGG GTT CTT GAC AAT GGT 1512
Lys Asn Gly Gly Pro Val Asp Ile His Arg Val Leu Asp Asn Gly
460 465 470

CTC TTA GTG GAT CCC CAT GAT CAG CAG GCA ATT GCT GAT GCT CTT 1557
Leu Leu Val Asp Pro His Asp Gln Gln Ala Ile Ala Asp Ala Leu
475 480 485

TTG AAG TTG GTT GCT GAT AAG CAA CTG TGG GCT AAA TGC AGG GCA 1602
Leu Lys Leu Val Ala Asp Lys Gln Leu Trp Ala Lys Cys Arg Ala
490 495 500

AAT GGA TTA AAA AAT ATC CAC CTT TTC TCA TGG CCC GAG CAC TGT 1647
Asn Gly Leu Lys Asn Ile His Leu Phe Ser Trp Pro Glu His Cys
505 510 515

AAA ACT TAT CTA TCC CGG ATA GCT AGC TGC AAA CCG AGG CAA CAT 1692
Lys Thr Tyr Leu Ser Arg Ile Ala Ser Cys Lys Pro Arg Gln His
520 525 530

TCC TTG AGA GAT ATT CAT GAT ATA TCT CTG AAT TTG AGA TTT TCA 1737
Ser Leu Arg Asp Ile His Asp Ile Ser Leu Asn Leu Arg Phe Ser
535 540 540

TTA GAT GGG GAA AAG AAT GAC AAT AAA GAA AAT GCT GAT AAT ACA 1782
Leu Asp Gly Glu Lys Asn Asp Asn Lys Glu Asn Ala Asp Asn Thr
545 550 555

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TTA GAC CCC GAA GTT CGA AGG AGC AAG TTA GAG AAT GCT GTT TTG      1827
Leu Asp Pro Glu Val Arg Arg Ser Lys Leu Glu Asn Ala Val Leu
                560                 565                 570

TCC TTA TCT AAG GGT GCA CTG AAG AGC ACA TCA AAA TCT TGG TCG      1872
Ser Leu Ser Lys Gly Ala Leu Lys Ser Thr Ser Lys Ser Trp Ser
                575                 580                 585

TCA GAC AAG GCA GAC CAA AAT CCT GGT GCT GGT AAA TTC CCA GCG      1917
Ser Asp Lys Ala Asp Gln Asn Pro Gly Ala Gly Lys Phe Pro Ala
                590                 595                 600

ATT AGG AGG AGG CGA CAT ATT TTT GTT ATT GCA GTG GAT TGT GAT      1962
Ile Arg Arg Arg Arg His Ile Phe Val Ile Ala Val Asp Cys Asp
                605                 610                 615

GCT AGC TCA GGA CTC TCT GGA AGT ATG AAA AAG ATA TTT GAG GCT      2007
Ala Ser Ser Gly Leu Ser Gly Ser Met Lys Lys Ile Phe Glu Ala
                620                 625                 630

GTA GAG AAG GAA AGG GCA GAG GGT TCC ATT GGA TTT ATC CTT GCT      2052
Val Glu Lys Glu Arg Ala Glu Gly Ser Ile Gly Phe Ile Leu Ala
                635                 640                 645

ACA TCT TTC AAT ATA TCA GAA GTA CAG TCT TTC CTG CTT TCA GAG      2097
Thr Ser Phe Asn Ile Ser Glu Val Gln Ser Phe Leu Leu Ser Glu
                650                 655                 660

GGC ATG AAT CCT ACT GAG CAA AAT CCT TTT GTA GTT GAC TTG TAC      2142
Gly Met Asn Pro Thr Glu Gln Asn Pro Phe Val Val Asp Leu Tyr
                665                 670                 675

TAT CAC TCA CAT ATT GAG TAT CGT TGG GGG GGC GAA GGG TTG AGA      2187
Tyr His Ser His Ile Glu Tyr Arg Trp Gly Gly Glu Gly Leu Arg
                680                 685                 690
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AAG ACT TTG GTG CGT TGG GCC GCC TCT ATC ATT GAT AAG AAT GGT      2232
Lys Thr Leu Val Arg Trp Ala Ala Ser Ile Ile Asp Lys Asn Gly
                695                 700                 705

GAA AAT GGA GAT CAC ATT GTT GTT GAG GAT GAA GAC AAT TCA GCT      2277
Glu Asn Gly Asp His Ile Val Val Glu Asp Glu Asp Asn Ser Ala
                710                 715                 720

GAC TAC TGC TAT ACA TTC AAA GTT TGC AAG CCT GGG ACG GTT CCT      2322
Asp Tyr Cys Tyr Thr Phe Lys Val Cys Lys Pro Gly Thr Val Pro
                725                 730                 735

CCA TCT AAA GAA CTT AGA AAA GTA ATG CGA ATT CAG GCA CTT CGT      2367
Pro Ser Lys Glu Leu Arg Lys Val Met Arg Ile Gln Ala Leu Arg
                740                 745                 750

TGT CAC GCT GTT TAT TGT CAA AAT GGG AGT AGG ATT AAT GTG ATC      2412
Cys His Ala Val Tyr Cys Gln Asn Gly Ser Arg Ile Asn Val Ile
                755                 760                 765

CCT GTA CTG GCA TCT CGG TCC CAA GCA CTC AGG TAC TTA TAT CTG      2457
Pro Val Leu Ala Ser Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Leu
                770                 775                 780

CGA TGG GGA ATG GTC CCT GTA CTG GCA TCT CGG TCC CAA GCA CTC      2502
Arg Trp Gly Met Val Pro Val Leu Ala Ser Arg Ser Gln Ala Leu
                785                 790                 795

AGG TAC TTA TAT CTG CGA TGG GGA ATG GTC CCT GTA CTG GCA TCT      2547
Arg Tyr Leu Tyr Leu Arg Trp Gly Met Val Pro Val Leu Ala Ser
                800                 805                 810

CGG TCC CAA GCA CTC AGG TAC TTA TAT CTG CGA TGG GGA ATG GAC      2592
Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Leu Arg Trp Gly Met Asp
                815                 820                 825
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TTG TCG AAG TTG GTG GTT TTC GTC GGA GAA AGT GGT GAT ACC GAT      2637
Leu Ser Lys Leu Val Val Phe Val Gly Glu Ser Gly Asp Thr Asp
          830                 835                 840

TAT GAA GGA TTG ATC GGT GGT CTA CGC AAG GCT GTC ATA ATG AAA      2682
Tyr Glu Gly Leu Ile Gly Gly Leu Arg Lys Ala Val Ile Met Lys
          845                 850                 855

GGA CTC TGC ACT AAT GCA AGC AGC TTA ATT CAC GGT AAT AGG AAT      2727
Gly Leu Cys Thr Asn Ala Ser Ser Leu Ile His Gly Asn Arg Asn
          860                 865                 870

TAC CCG CTA TCT GAT GTT TTA CCA TTC GAG AGC CCT AAT GTC ATC      2772
Tyr Pro Leu Ser Asp Val Leu Pro Phe Glu Ser Pro Asn Val Ile
          875                 880                 885

CAA GCG GAT GAG GAA TGT AGC AGC ACC GGA ATC CGT TCC TTA CTG      2817
Gln Ala Asp Glu Glu Cys Ser Ser Thr Gly Ile Arg Ser Leu Leu
          905                 910                 915

GAG AAA CTA GCG GTA CTC AAA GGA TAA TACCCTTCCC CCTTTGATTG        2864
Glu Lys Leu Ala Val Leu Lys Gly End
          920

TCAAAAACCT ATATGAGCTA AGATTATGCC ATGAAAAGAA TGGCCATCCA TTTGGCTTGT2924

CTTTTG  2930
```

4. Derivatives of DNA sequences according to any one of claims 1 to 3, characterised in that these derivatives are obtained by exchange of single bases or by deletion or insertion of base sequences and which code for proteins with a comparable activity to sucrose phosphate synthase.

to 7 for the preparation of plants with changed sucrose concentration.

10. Use of the plasmid p35S-anti-pot-SPS for the preparation of plants with reduced mRNA concentration for the SPS protein and reduced enzyme activity.

11. Use of the plasmid p35S-anti-pot-SPS for the preparation of plants with reduced mRNA concentration for the SPS protein and reduced enzyme activity, specifically in the tuber.

12. Use of the DNA sequences according to any one of claims 1 to 3 for the preparation of derivatives by targeted or non-targeted mutagenesis.

13. Use of the DNA sequences according to any one of claims 1 to 3 for the preparation of derivatives, whose gene products are not subjected to the plant's own activity regulation during a phosphorylation reaction.

14. Use of the DNA sequences according to any one of claims 1 to 3 for the preparation of derivatives, whose gene products are not neutralized by the plant's own activity regulation during a phosphorylation reaction.

15. Transgenic plants, whose sugar metabolism is modified by introduction of one or several of the DNA sequences according to any one of claims 1 to 3.

16. Plants according to claim 15, characterised in that it is a potato.

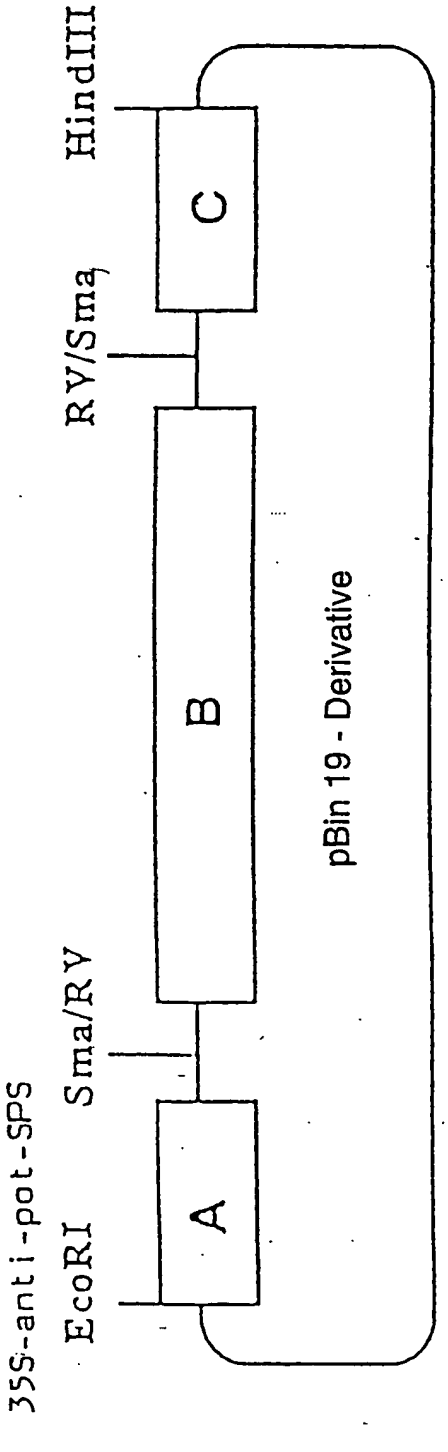
35S-anti-pot-SPS
EcoRI
Sma/RV
Sma/RV
HindIII
A
B
C
pBin 19 - Derivative

Fig. 1

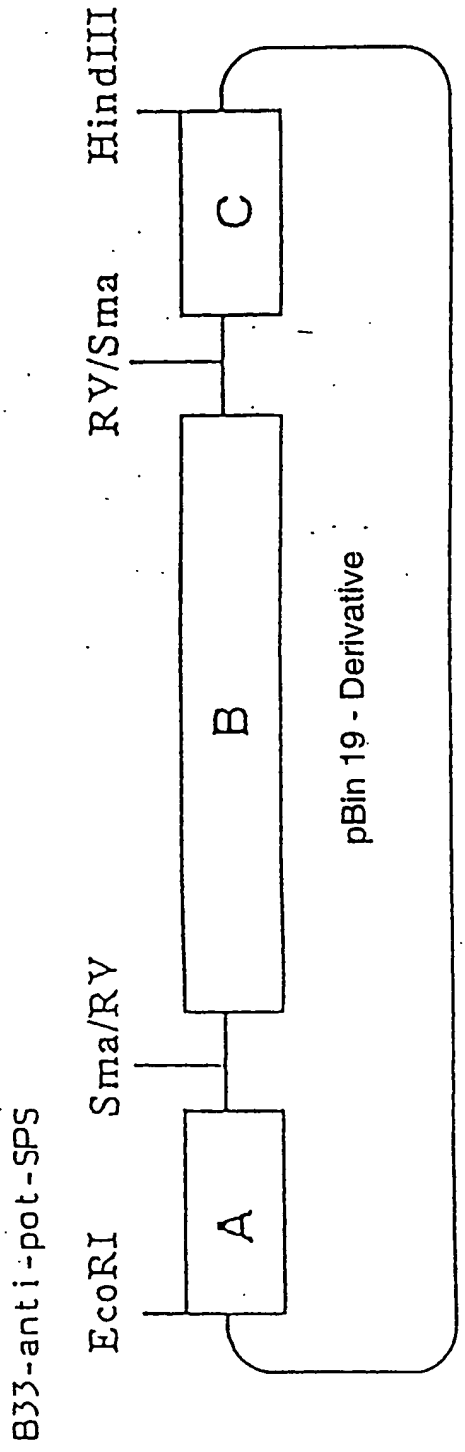
B33-anti-pot-SPS
EcoRI
Sma/RV
Sma/RV
HindIII
A
B
C
pBin 19 - Derivative

Fig. 2

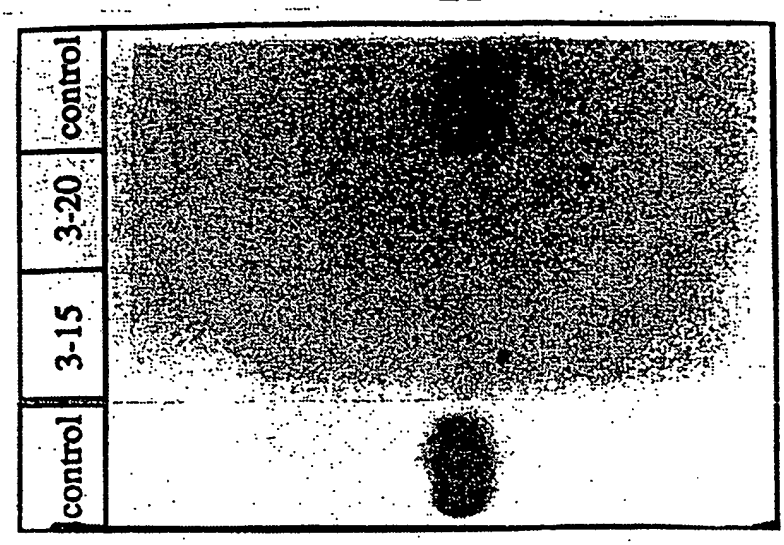
control
3-15
3-20
control

Fig. 4


control
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1-74
1-75

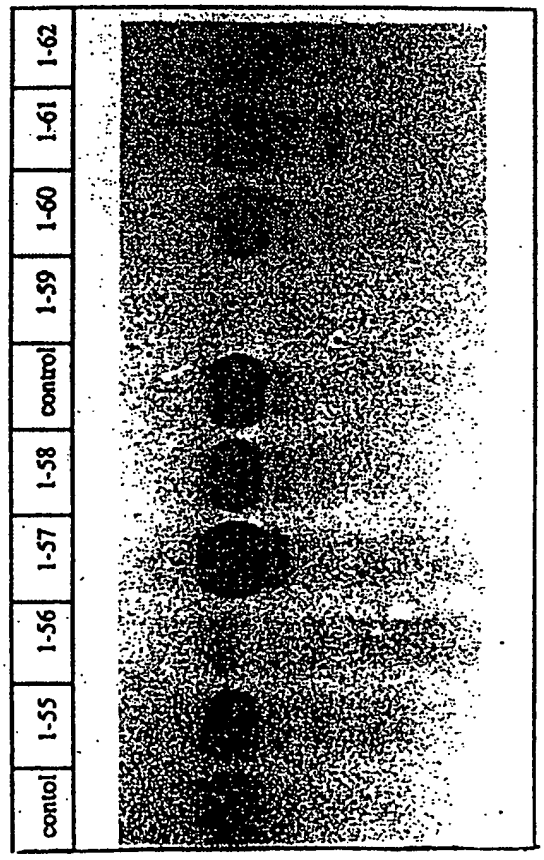
contol
1-55
1-56
1-57
1-58
control
1-59
1-60
1-61
1-62

Fig. 3

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

Institut für Genbiologische
Forschung Berlin GmbH
Ihnestrasse 63
1000 Berlin 33

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR pB33-anti-pot-sps	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 7124

II. SCIENTIFIC DESCRIPTION AND/OR TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

( ) a scientific description
( ) a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts this microorganism identified under I. above, which was received by it on 1992-06-12 (Date of original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I above was received by this International Depositary Authority on (date of original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: DSM-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Adress: Mascheroder Weg 1 B D-3300 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): U. Weiss Date: 1992-06-30

[1] Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

Form DSM BP/4 (sole page) 0391

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

Institut für Genbiologische
Forschung Berlin GmbH
Ihnestrasse 63
1000 Berlin 33

VIABILITY STATEMENT
issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Institut für Genbiologische Forschung Berlin GmbH Address: Ihnestrasse 63 1000 Berlin 33	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 7124 Date of the deposit or of the transfer[1]: 1992-06-12

III. VIABILITY STATEMENT

The viability of the microorganism identified under II above was tested on 1992-06-15 .[2]
On that date, the said microorganism was

(X)[3] viable

( )[3] no longer viable

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED[4]

IV. INTERNATIONAL DEPOSITARY AUTHORITY

Name: DSM DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Mascheroder Weg 1 B D-3300 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): U. Weiss Date: 1992-06-30

1 Indicate the date of original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).

2 In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.

3 Mark with a cross the applicable box.

4 Fill in if the information has been requested and if the results of the test were negative.

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

Institut für Genbiologische
Forschung Berlin GmbH
Ihnestrasse 63
1000 Berlin 33

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR p35S-anti-pot-sps	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 7125

II. SCIENTIFIC DESCRIPTION AND/OR TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

( ) a scientific description
( ) a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts this microorganism identified under I. above, which was received by it on 1992-06-12 (Date of original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I above was received by this International Depositary Authority on (date of original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: DSM-DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Adress: Mascheroder Weg 1 B D-3300 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): U. Weiss Date: 1992-06-30

[1] Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

Institut für Genbiologische
Forschung Berlin GmbH
Ihnestrasse 63
1000 Berlin 33

VIABILITY STATEMENT
issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: Institut für Genbiologische Forschung Berlin GmbH Address: Ihnestrasse 63 1000 Berlin 33	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: DSM 7125 Date of the deposit or of the transfer[1]: 1992-06-12

III. VIABILITY STATEMENT

The viability of the microorganism identified under II above was tested on 1992-06-15 .[2]
On that date, the said microorganism was

(X)[3] viable

( )[3] no longer viable

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED[4]

IV. INTERNATIONAL DEPOSITARY AUTHORITY

Name: DSM DEUTSCHE SAMMLUNG VON MIKROORGANISMEN UND ZELLKULTUREN GmbH Address: Mascheroder Weg 1 B D-3300 Braunschweig	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): U. Weiss Date: 1992-06-30

1 Indicate the date of original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).

2 In the cases referred to in Rule 10.2(a) (ii) and (iii), refer to the most recent viability test.

3 Mark with a cross the applicable box.

4 Fill in if the information has been requested and if the results of the test were negative.

Form DSM-BP/9 (sole page) 0787

INTERNATIONAL SEARCH REPORT

Inter. nal Application No
PCT/EP 93/01605

A. CLASSIFICATION OF SUBJECT MATTER
IPC 5 C12N9/10 C12N15/82 C12N15/11 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 5 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	THE PLANT CELL. vol. 3, no. 10 , October 1991 , ROCKVILLE, MD, USA. pages 1121 - 1130 WORRELL, A.C., ET AL. 'Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohydrate partitioning'	5,9
Y	see the whole document ---	5,9
X	THE PLANT JOURNAL vol. 1, no. 1 , 1991 pages 51 - 58 QUICK, W.P., WT AL. 'The impact of decreased Rubisco on photosynthesis,growth, allocation and storage in tobacco plants which have been transformed with antisense rbcS' see the whole document ---	5,9

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 November 1993	12. 93

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016	MADDOX, A

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	PLANT PHYSIOLOGY. vol. 99, no. 1 , May 1992 , ROCKVILLE, MD, USA. page 12 SONNEWALD, U., ET AL. 'Molecular approaches to influence sink-source interactions in transgenic plants' see abstract 67	5,9
X	EP,A,0 438 904 (ADVANCED TECHNOLOGIES) 31 July 1991 see page 7, line 40 - line 60	5,9
X	EP,A,0 485 044 (IGFB) 13 May 1992 see the whole document	5,9
X	EP,A,0 466 995 (ROUSSEL-UCLAF) 22 January 1992 see the whole document	5
P,X	WO,A,92 16631 (ROUSSEL-UCLAF) 1 October 1992 see the whole document	5,9
P,X	EP,A,0 530 978 (ADVANCED TECHNOLOGIES) 10 March 1993 see the whole document	5,9
A	EP,A,0 455 316 (IGFB) 6 November 1991 see the whole document	1-16
A	BIOLOGICAL ABSTRACTS vol. 55 1973, Philadelphia, PA, US; abstract no. 68960, MURATA, T. 'Sucrose phosphate synthetase from various plant origins' see abstract & AGRIC. BIOL. CHEM. vol. 36, no. 11 , 1972 pages 1877 - 1884	1-16
A	BIOLOGICAL ABSTRACTS vol. 80 1985, Philadelphia, PA, US; abstract no. 85644, SOWOKINOS, J.R., ET AL. 'Translucent tissue defects in Solanum tuberosum: 1. Alterations in amyloplast membrane integrity, enzyme activities, sugars and starch content' see abstract & PLANT PHYSIOL vol. 78, no. 3 , 1985 pages 489 - 494	1-16

INTERNATIONAL SEARCH REPORT

...information on patent family members

Inten nal Application No
PCT/EP 93/01605

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
EP-A-0438904	31-07-91	AU-A-	6836590	04-07-91
		JP-A-	4341126	27-11-92
EP-A-0485044	13-05-92	DE-A-	4035756	14-05-92
		AU-A-	8702191	14-05-92
		CA-A-	2055150	09-05-92
EP-A-0466995	22-01-92	AU-A-	8394591	18-02-92
		WO-A-	9201782	06-02-92
		JP-T-	5502169	22-04-93
WO-A-9216631	01-10-92	AU-A-	8765591	21-10-92
		EP-A-	0533849	31-03-93
EP-A-0530978	10-03-93	NONE		
EP-A-0455316	06-11-91	DE-A-	4013144	24-10-91

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